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82001

From: Schnizer, Holly
Sent: Tuesday, December 10, 2002 9:30 AM
To: STIC-Biotech/ChemLib
Subject: seq. search for appl. no. 09/444,281

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STIC-Biotech/ChemLib
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Please search the commercial and interference databases for:

SEQ ID NOs: 35 and 36 and,

a peptide with the following sequence (SEQ ID NO: 35)(SEQ ID NO:27)(SEQ ID NO:35)

Thank you.

Holly Schnizer
AU 1653
CM1-9E09
305-3722
mailbox: CM1-9B01

9E09

Searcher: Point of Contact
Phone: P. Sheppard
Location: Telephone number: (703) 308-4499
Date Picked Up: _____
Date Completed: 12/13/02
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:

NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)

STN: _____
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 11, 2002, 15:37:24 ; Search time 28 seconds
(without alignments)
272.277 Million cell updates/sec

Title: US-09-444-281-35-27-35
Perfect score: 241
Sequence: 1 ILKKPMPWRKRKHEAPEPIMLKKPMPWRKR 37

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_21: *
1: sp.archaea: *
2: sp.bacteria: *
3: sp.fungi: *
4: sp.human: *
5: sp.invertebrate: *
6: sp.mammal: *
7: sp.mhc: *
8: sp.organelle: *
9: sp.phage: *
10: sp.plant: *
11: sp.todent: *
12: sp.virus: *
13: sp.vertebrate: *
14: sp.unclassified: *
15: sp.virus: *
16: sp.bacteriophage: *
17: sp.archae: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	70.5	29.3	1245	3	Q9Y7V5
2	67.5	28.0	746	12	Q9JH31
3	67	27.8	723	12	Q9DUC4
4	64	26.6	175	12	Q91RP8
5	63	26.1	49	12	Q9DTR0
6	63	26.1	192	16	Q928B7
7	63	26.1	748	12	Q9DTR1
8	63	26.1	750	11	Q91D04
9	62	25.7	367	11	Q63778
10	61	25.3	92	12	Q8V7E2
11	61	25.3	250	17	Q8TWG0
12	61	25.3	284	10	Q94CT8
13	61	25.3	734	12	Q8V7I1
14	61	25.3	735	12	Q9DUC9
15	61	25.3	985	15	Q98414
16	60	24.9	147	11	Q61427

17	60	24.9	242	17	Q8TVM8
18	60	24.9	381	16	Q9A7E1
19	60	24.9	766	12	Q91CY5
20	59.5	24.7	114	16	Q9X8C2
21	59.5	24.7	2292	12	Q66765
22	59	24.5	95	10	Q9LON0
23	59	24.5	485	16	P72844
24	59	24.5	739	12	Q99A03
25	58.5	24.3	521	10	Q94EP3
26	58.5	24.3	1567	2	Q9ADW1
27	58	24.1	107	16	Q9XAE4
28	58	24.1	513	11	Q63289
29	58	24.1	646	11	Q63779
30	58	24.1	879	11	Q8Y199
31	58	24.1	1300	11	P97692
32	57.5	23.9	117	15	Q9YR99
33	57.5	23.9	341	13	Q90644
34	57.5	23.9	376	3	Q94516
35	57.5	23.9	444	4	Q9HC40
36	57.5	23.9	772	4	Q9BXY6
37	57	23.7	252	15	Q91U37
38	57	23.7	426	12	Q99A07
39	57	23.7	970	11	Q88821
40	57	23.7	971	11	Q70458
41	56.5	23.4	157	5	Q9YOE8
42	56.5	23.4	162	5	Q9W1W7
43	56.5	23.4	532	16	Q9CK19
44	56	23.2	252	15	Q91TX8
45	56	23.2	252	15	Q91TV2

ALIGNMENTS

RESULT 1	
ID Q9Y7V5	PRELIMINARY; PRT; 1245 AA.
AC Q9Y7V5;	
DT 01-NOV-1999 (TREMBLrel. 12, Created)	
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)	
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)	
DE Condiospore surface protein.	
GN Cmpl.	
OS Trichoderma harzianum.	
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;	
OC Hypocreales; Mitosporic Hypocreales; Trichoderma.	
OX NCBI_TaxID=5544;	
RN [1]	
RP SEQUENCE FROM N.A.	
RC STRAIN=ATCC 32173;	
RX MEDLINE=99343861; PubMed=10413618;	
RA Puyesky M., Benhamou N., Ponce Noyola P., Bauw G., Ziv T.,	
RA Van Montagu M., Herrera Estrella A., Horwitz B.A.;	
RT "Developmental regulation of cmlp, a gene encoding a multidomain	
RT Condiospore surface protein of Trichoderma.";	
RL Fungal Genet. Biol. 27:88-99(1999).	
DR EMBL; AJ133651; CAB40845.1; -	
DR HSSP; P01180; INPO.	
DR InterPro; IPR001832; Claudin.	
DR InterPro; IPR001673; S.mold.repeat.	
DR Prodom; PD006869; S.mold.repeat. 2.	
DR PROSITE; PS01346; CLAUDIN; UNKNOWN_1.	
SQ SEQUENCE 1245 AA; 135824 MW; 3249C749AFAOCDP8 CRC64;	
Query Match	29.3%; Score 70.5; DB 3; Length 1245;
Best Local Similarity	29.0%; Pred. No. 2.3;
Matches	9; Conservative 2; Mismatches 9; Indels 11; Gaps 1;
QY 4 KRPMPWRKRKHEAPEPIMLKKPMPWR 34	
DB 1185 RMOQMSWPRRGRC-----CWQMSW 1204	

RESULT 2

09JH31 PRELIMINARY: PRT: 746 AA.
 AC 09JH31;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE ORF1.
 OS TT virus.
 OC Viruses; ssDNA viruses; unclassified ssDNA viruses.
 OX NCBI_TaxID=68887;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TJN02;
 RA Okamoto H.;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TJN02;
 RA MEDLINE=20456801; PubMed=11003468;
 RA Ukita M., Okamoto H., Nishizawa T., Tawara A., Takahashi M.,
 RA Itzuka H., Miyakawa Y., Mayumi M.;
 RA "The entire nucleotide sequences of two distinct TT virus (TTV)
 RA isolates (TJN01 and TJN02) remotely related to the original TTV
 RA isolates.";
 RL Arch. Virol. 145:1543-1559(2000).
 DR EMBL; AB028669; BAA94878.1; -;
 DR InterPro; IPR004219; TTVirus_Unk.
 DR Pfam; PF02956; TT_ORF1.1.
 SQ SEQUENCE 746 AA; 88561 MW; E0B22953AE764E3E CRC64;

Query Match

Best Local Similarity 28.0%; Score 67.5; DB 12; Length 746;
 Matches 11; Conservative 2; Mismatches 5; Indels 15; Gaps 1;

OY 5 WPWMPWRKHHEAPEPIMILKKWMPWRRK 37
 | | | | |
 Db 3 WGMWRRRR-----RWPARRRRR 20

RESULT 3

09DU04 PRELIMINARY: PRT: 723 AA.

AC 09DU04;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE ORF1.
 OS TT virus.
 OC Viruses; ssDNA viruses; unclassified ssDNA viruses.
 OX NCBI_TaxID=68887;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MF-TTV9;
 RA Okamoto H.;
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MF-TTV9;
 RA MEDLINE=20534983; PubMed=11080484;
 RA Okamoto H., Nishizawa T., Tawara A., Peng Y., Takahashi M.,
 RA Kishimoto J., Tanaka T., Miyakawa Y., Mayumi M.;
 RA "Species-specific TT viruses in humans and nonhuman primates and their
 RA phylogenetic relatedness.";
 RL Virology 277:368-378(2000).
 DR EMBL; AB041959; BAB19313.1; -;
 DR InterPro; IPR001563; Serine_carboxypept.
 DR Pfam; PF02956; TT_ORF1.1.
 DR PROSITE; PS00131; CARBOXYPEPT_SRR_SRR; UNKNOWN_1.
 SQ SEQUENCE 723 AA; 85393 MW; 232D003098766544 CRC64;

Query Match

27.8%; Score 67; DB 12; Length 723;

Best Local Similarity 34.4%; Pred. No. 3.6;
 Matches 11; Conservative 1; Mismatches 2; Indels 18; Gaps 1;

OY 6 PWWMPWRKHHEAPEPIMILKKWMPWRRK 37
 | | | | |
 Db 2 PWWMPWR-----WRRWRRR 15

RESULT 4

091RD8 PRELIMINARY: PRT: 175 AA.

AC 091RD8;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE ORF3.
 OS TT virus.
 OC Viruses; ssDNA viruses; unclassified ssDNA viruses.
 OX NCBI_TaxID=68887;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=L03;
 RA Liu Z.H., Luo K.X., Hu J., He H.T.;
 RA Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AF371370; AAK54733.1; -;
 DR InterPro; IPR004219; TTVirus_Unk.
 DR Pfam; PF02956; TT_ORF1.1.
 SQ SEQUENCE 175 AA; 22073 MW; 5212D7DA3FD72F81 CRC64;

Query Match

Best Local Similarity 26.6%; Score 64; DB 12; Length 175;
 Matches 11; Conservative 2; Mismatches 4; Indels 16; Gaps 2;

OY 5 WPWMPWRKHHEAPEPIMILKKWMPWRRK 37
 | | | | |
 Db 3 WSWW-WRRRR-----WMPRRRR 19

RESULT 5

09DT80 PRELIMINARY: PRT: 49 AA.

AC 09DT80;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE ORF1 (Fragment).
 OS TT virus.
 OC Viruses; ssDNA viruses; unclassified ssDNA viruses.
 OX NCBI_TaxID=68887;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TYM9;
 RA MEDLINE=20568739; PubMed=11118348;
 RA Okamoto H., Nishizawa T., Tawara A., Takahashi M., Kishimoto J.,
 RA "TT virus, Sugai Y.;
 RA "TT virus mRNAs detected in the bone marrow cells from an infected
 RA individual.";
 RL Biochem. Biophys. Res. Commun. 279:700-707(2000).
 DR EMBL; AB050449; BAB19930.1; -;
 DR NON_TER 49
 FT SEQUENCE 49 AA; 7225 MW; 1DA6F8F1AB69AA43 CRC64;

Query Match

Best Local Similarity 26.1%; Score 63; DB 12; Length 49;
 Matches 10; Conservative 3; Mismatches 4; Indels 16; Gaps 2;

OY 5 WPWMPWRKHHEAPEPIMILKKWMPWRRK 37
 | | | | |
 Db 3 WTWW-WRRRR-----WMPRRR 19

RESULT 6

09Z8B7

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* ID 092887 PRELIMINARY; PRT; 192 AA.
AC 092887;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE C1277 STIMILARITY (CPJ0426 protein).
GN CPN0426 OR CPJ0426 OR CPJ327.
OS Chlamydia pneumoniae (Chlamydia pneumoniae).
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83558;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CML029;
RX MEDLINE=99206606; PubMed=10192388;
RA Kaldan S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.,
RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.",
RL Nat. Genet. 21:385-389(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AR39;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J., Uetzerback T., Berry K., Bass S.,
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA Eisen J., Nelson W., Deboy R., Kolonay J., McClarty G., Salzberg S.L.,
RA Giesen J., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis Mopn and Chlamydia
RT pneumoniae AR39.",
RL Nucleic Acids Res. 28:1397-1406(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=J138;
RX MEDLINE=20330349; PubMed=10871362;
RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
RA Shiba T., Ishii K., Hattori M., Kunara S., Nakazawa T.;
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
RT from Japan and CML029 from USA.",
RL Nucleic Acids Res. 28:2311-2314(2000).
DR EMBL: AE001625; AAD18570.1; -
DR EMBL: AE002194; AAF38182.1; -
DR EMBL: AP002546; BAA98634.1; -
DR TIGR: CP0327; -
KM Complete proteome.
SQ SEQUENCE 192 AA; 21464 MW; 9C38C329AEDDB76F CRC64;

Query Match 26.1%; Score 63; DB 16; Length 192;
Best Local Similarity 42.3%; Pred. No. 3;
Matches 11; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

OY 5 WPMWPMRRKHAEPEAPIMILKKWP 30
Db 138 WPMWPMRRKHAEPEAPIMILKKWP 163

RESULT 7
O92881 PRELIMINARY; PRT; 748 AA.
AC 092881;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE ORE1.
OS TT virus.
OC Viruses; ssDNA viruses; unclassified ssDNA viruses.
OX NCBI_TaxID=68887;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TYM9;
RX MEDLINE=20568739; PubMed=11118348;
RA Okamoto H., Nishizawa T., Tawara A., Takahashi M., Kishimoto J.,
RA Sai T., Sugai Y.;
RT "TT virus mRNAs detected in the bone marrow cells from an infected
RT

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RT Individual.";
RL Biochem. Biophys. Res. Commun. 279:700-707(2000).
DR EMBL: AB050448; BAB19928.1; -
DR InterPro: IPR004219; TTVirus_Unk.
DR Pfam: PF02956; TT_ORF1; 1.
SQ SEQUENCE 748 AA; 88552 MW; D6SCCB2CMA5CE26F CRC64;

Query Match 26.1%; Score 63; DB 12; Length 748;
Best Local Similarity 30.3%; Pred. No. 11;
Matches 10; Conservative 3; Mismatches 4; Indels 16; Gaps 2;

OY 5 WPMWPMRRKHAEPEAPIMILKKWPMWRRK 37
Db 3 WPMWPMRRKHAEPEAPIMILKKWPMWRRK 19

RESULT 8
O91D04 PRELIMINARY; PRT; 750 AA.
AC 091D04;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE ORE1.
OS TT virus.
OC Viruses; ssDNA viruses; unclassified ssDNA viruses.
OX NCBI_TaxID=68887;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21488921; PubMed=11601907;
RA Okamoto H., Nishizawa T., Takahashi M., Asabe S., Tsuda F.,
RA Yoshikawa A.;
RT "Heterogeneous distribution of TT virus of distinct genotypes in
RT multiple tissues from infected humans.";
RL Virology 288:358-368(2001).
DR EMBL: AB060592; BAB69900.1; -
DR InterPro: IPR004219; TTVirus_Unk.
DR Pfam: PF02956; TT_ORF1; 1.
SQ SEQUENCE 750 AA; 89223 MW; 616EC86DC3469091 CRC64;

Query Match 26.1%; Score 63; DB 12; Length 750;
Best Local Similarity 30.3%; Pred. No. 11;
Matches 10; Conservative 3; Mismatches 4; Indels 16; Gaps 2;

OY 5 WPMWPMRRKHAEPEAPIMILKKWPMWRRK 37
Db 3 WPMWPMRRKHAEPEAPIMILKKWPMWRRK 19

RESULT 9
O63778 PRELIMINARY; PRT; 367 AA.
AC 063778;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE Hypothetical 43.7 kDa protein.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=87064324; PubMed=3023845;
RA D'Ambrósio E., Walzkin S.D., Wilney F.R., Saleme A., Furano A.V.;
RT "Structure of the highly repeated, long interspersed DNA family (LINE
RT or L1rn) of the rat.";
RL Mol. Cell. Biol. 6:411-424(1986).
DR EMBL: M13100; AAA6046.1; -
DR InterPro: IPR000566; LipoCln_cyFAP.
DR PROSITE: PS00213; LIPOCALIN; UNKNOWN_1.
KM Hypothetical protein.

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SQ SEQUENCE 367 AA; 43685 MW; 4654499CC185EC3B CRC64;

Query Match 25.7%; Score 62; DB 11; Length 367;

Best Local Similarity 39.4%; Pred. No. 7.4; Mismatches 13; Conservative 4; Indels 12; Gaps 4; 2;

OY 1 ILKKPMPWPR--RKHEAPEAPIMILK-KW 29
 Db 25 IFSKWCWFNRATCRMQIDPISLSPCTKLKSKW 57

RESULT 10

08V7E2 PRELIMINARY; PRT; 92 AA.

AC 08V7E2; MEDLINE=2184401; PubMed=11855633;

DT 01-MAR-2002 (TRENBLrel. 20, Created)

DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)

DE 01-JUN-2002 (TRENBLrel. 21, Last annotation update)

OS ORF1 (Fragment).

OC TT virus.

OC Viruses; ssDNA viruses; unclassified ssDNA viruses.

OX NCBI_TaxID=68887;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=2184401; PubMed=11855633;

RA Peng Y.H., Nishizawa T., Takahashi M., Ishikawa T., Yoshikawa A.,

RT Okamoto H.;

RT "Analysis of the complete genomes of thirteen TT virus variants

RT classifiable into the fourth and fifth genetic groups, isolated from

RT viremic infants."

RL Arch. Virol. 147:21-41(2002).

DR EMBL; AB064615; BAB79374.1; -.

DR InterPro: IPR004219; TTVirus-Unk.

DR Pfam: PF02956; TT_ORF1.1.

FT NON_TER 92

SQ SEQUENCE 92 AA; 12429 MW; 188D83D05A7B09A CRC64;

Query Match

Best Local Similarity 25.3%; Score 61; DB 12; Length 92;

Matches 10; Conservative 3; Mismatches 2; Indels 16; Gaps 1;

OY 7 WMPWRKHEAPEAPIMILKKPMPWPRK 37

Db 3 WMPWRKHEAPEAPIMILKKPMPWPRK 17

RESULT 11

08TWG0 PRELIMINARY; PRT; 250 AA.

AC 08TWG0; MEDLINE=21927647; PubMed=11930014;

DT 01-JUN-2002 (TRENBLrel. 21, Created)

DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)

DE 01-JUN-2002 (TRENBLrel. 21, Last annotation update)

OS NAD-dependent protein deacetylase, STR2 family.

GN SIR2 OR MK1075.

OS Methanopyrus kandleri.

OC Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;

OC Methanopyrus.

OX NCBI_TaxID=2320;

RN [1]

RP SEQUENCE FROM N.A.

RX STRAIN=AV19 / DSM 6324 / JCM 9639;

RA MEDLINE=21927647; PubMed=11930014;

RA Slesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N.,

RA Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,

RA Natale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,

RA Malysk A.G., Koonin E.V., Kozlovskiy S.A.; Methanopyrus kandleri AV19

RT "The complete genome of hyperthermophilic Methanopyrus kandleri AV19

RT and monophyly of archaeal methanogens."

RT Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).

DR EMBL; AE010396; AAM02288.1; -.

DR Complete proteome.

SQ SEQUENCE 250 AA; 27799 MW; B051994FE5B24E05 CRC64;

Query Match 25.3%; Score 61; DB 17; Length 250;

Best Local Similarity 50.0%; Pred. No. 6.7;

Matches 10; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

OY 3 KKPMPWRKHEAPEAPIMILKKPMPWPRK 22

Db 60 KKPMPWRKHEAPEAPIMILKKPMPWPRK 79

RESULT 12

094C18 PRELIMINARY; PRT; 284 AA.

AC 094C18; MEDLINE=2184401; PubMed=11855633;

DT 01-DEC-2001 (TRENBLrel. 19, Created)

DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)

DE 01-DEC-2001 (TRENBLrel. 19, Last annotation update)

OS Lycopersicon esculentum (Tomato).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

OX NCBI_TaxID=4081;

RN [1]

RP SEQUENCE FROM N.A.

RA Uthappa M., Muchhal U.S., Baldwin J.C., Raghothama K.G.;

RT "LeGRP1, A new member of glycine-rich proteins from tomato

RT (Lycopersicon esculentum)."

RL Physiol. Plantarum 0:0-0(2001).

DR EMBL; AY026037; AAK08984.1; -.

SQ SEQUENCE 284 AA; 23434 MW; E81A84C247C9BED8 CRC64;

Query Match

Best Local Similarity 25.3%; Score 61; DB 10; Length 284;

Matches 10; Conservative 0; Mismatches 4; Indels 18; Gaps 2;

OY 5 WMPWRKHEAPEAPIMILKKPMPWPRK 36

Db 9 WMPWRKHEAPEAPIMILKKPMPWPRK 22

RESULT 13

08V7I1 PRELIMINARY; PRT; 734 AA.

AC 08V7I1; MEDLINE=2184401; PubMed=11855633;

DT 01-MAR-2002 (TRENBLrel. 20, Created)

DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)

DE 01-JUN-2002 (TRENBLrel. 21, Last annotation update)

OS TT virus.

OC Viruses; ssDNA viruses; unclassified ssDNA viruses.

OX NCBI_TaxID=68887;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CT43F;

RA Peng Y.H., Nishizawa T., Takahashi M., Ishikawa T., Yoshikawa A.,

RA Okamoto H.;

RA Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RX STRAIN=CT43F;

RA MEDLINE=2184401; PubMed=11855633;

RA Peng Y.H., Nishizawa T., Takahashi M., Ishikawa T., Yoshikawa A.,

RA Okamoto H.;

RA "Analysis of the complete genomes of thirteen TT virus variants

RT classifiable into the fourth and fifth genetic groups, isolated from

RT viremic infants."

RL Arch. Virol. 147:21-41(2002).

DR EMBL; AB064598; BAB79322.1; -.

DR InterPro: IPR004219; TTVirus-Unk.

DR Pfam: PF02956; TT_ORF1.1.

SQ SEQUENCE 734 AA; 86978 MW; F60E188BC0104A68 CRC64;

Query Match

25.3%; Score 61; DB 12; Length 734;

Best Local Similarity 32.3%; Pred. No. 19;
Matches 10; Conservative 3; Mismatches 2; Indels 16; Gaps 1;

Oy 7 WMPWRKHAEPEAEPIMLKKMPWRRK 37
Db 3 WMYRRR-----PWRRRRR 17

RESULT 14

O9DUC9 PRELIMINARY; PRT; 735 AA.

AC O9DUC9;

DT 01-MAR-2001 (TREMblrel. 16, Created)

DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)

DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)

DE ORF1.

OS TT virus.

OC Viruses; ssDNA viruses; unclassified ssDNA viruses.

OX NCBI_Taxid=68887;

RN [1]

RP SEQUENCE FROM N.A.

RA STRAIN-PT-TTV6;

RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RA STRAIN-PT-TTV6;

RX MEDLINE-20534983; PubMed=11080484;

RA Okamoto H., Nishizawa T., Tawara A., Peng Y., Takahashi M.,

RA Kishimoto J., Tanaka T., Miyakawa Y., Mayumi M.;

RT "Species-specific TT viruses in humans and nonhuman primates and their

RT phylogenetic relatedness";

RL Virology 277:368-378(2000).

RL EMBL, AB041957; BAB19308.1;

DR InterPro: IPR004219; TTVirus_Unk.

DR Pfam: PF02956; TT_ORF1.1.

DR SEQUENCE 735 AA; 86132 MW; 9ED818DBE6FA5D3 CRC64;

Query Match 25.3%; Score 61; DB 12; Length 735;

Best Local Similarity 29.3%; Pred. No. 19;

Matches 12; Conservative 3; Mismatches 6; Indels 20; Gaps 3;

Oy 5 WPM-----WPMRKHAEPEAEPIMLKKMPW---PWRRK 37

Db 3 WPMRRRRRRRRRR-----PWRRRRRRRRRTT 31

RESULT 15

O98414 PRELIMINARY; PRT; 985 AA.

AC O98414;

DT 01-FEB-1997 (TREMblrel. 02, Created)

DT 01-FEB-1997 (TREMblrel. 02, Last sequence update)

DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)

DE Envelope glycoprotein.

GN ENV.

OS Ovine lentivirus.

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI_Taxid=11663;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-85/34;

RX MEDLINE-95135990; PubMed=7834396;

RA Woodward T.M., Carlson J.O., de la Concha-Bermejo A.,

RA Demartini J.C.;

RT "Biological and genetic changes in ovine lentivirus strains following

RT passage in isogeneic twin lambs";

RL J. Acquir. Immune Defic. Syndr. Hum. Retrovirol. 8:124-133(1995).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN-85/34;

RA Carlson J.O., Demartini J.C., Mwaengo D.M.;

RT "Envelope glycoprotein nucleotide sequence and genetic

RT characterization of North American ovine lentiviruses.";

RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.

DR EMBL: U64439; AAB08725.1;

DR InterPro: IPR000328; Env_GP41.

DR Pfam: PF00517; GP41; 1.

KW Transmembrane.

SO SEQUENCE 985 AA; 113794 MW; 3197258BDBE3597 CRC64;

Query Match 25.3%; Score 61; DB 15; Length 985;

Best Local Similarity 23.4%; Pred. No. 25;

Matches 18; Conservative 7; Mismatches 8; Indels 44; Gaps 5;

Oy 1 ILKK-----WP-----WPKRKHAEPEAE----- 21

Db 163 ILKRYKODWPNWYTHWPLMOMENRQMKENEREYKGTNTKEDIDDLAKIRGRFC 222

Oy 22 ---PIMLK--KMPWP 33

Db 223 VPPFPALKCTKWCWYP 239

Search completed: December 11, 2002, 15:39:39
Job time : 30 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 11, 2002, 15:34:48 ; Search time 11 Seconds

(without alignments)
139.511 Million cell updates/sec

Title: US-09-444-281-35-27-35

Perfect score: 241
Sequence: 1 ILKKMPWPMWRKHEPEAPIMILKKMPWPMWRK 37

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	78	32.4	144	1 INDC_BOVIN	P33046 bos taurus
2	62	25.7	314	1 YMA3_BACST	O45633 bacillus st
3	59.5	24.7	2290	1 P03304	P03304 encephalomy
4	57	23.7	711	1 MMLA-STRCO	O53902 streptomyc
5	55.5	23.0	55	1 ATP8_ANAPL	P50655 anas platyr
6	55.5	23.0	942	1 ENV_CAEGV	P31627 caprine art
7	55.5	23.0	990	1 ENV_OMVVS	P16899 ovine lenti
8	55	22.8	715	1 YD55_MYCTU	O11025 mycobacteri
9	54	22.4	144	1 AP22_APIME	P35881 apis mellif
10	54	22.4	469	1 STC1_MYCTU	P96862 mycobacteri
11	54	22.4	473	1 STC1_MYCTU	P57890 mycobacteri
12	54	22.4	1173	1 VGL2_CVH22	P15423 human coron
13	53.5	22.2	1042	1 COR1_HUMAN	O9y9q5 homo sapien
14	53.5	22.2	1113	1 COR1_HUMAN	O9y9q5 mus musculu
15	53	22.0	424	1 FDCG_SOYBN	P48628 glycine max
16	52.5	21.8	55	1 ATP8_AYTAM	O9xk25 aythya amer
17	52.5	21.8	257	1 E434_ADE40	O64665 human adeno
18	52.5	21.8	691	1 YHOG_ECOLI	P37645 escherichia
19	52.5	21.8	982	1 ENV_VILV	P03379 visna lenti
20	52.5	21.8	983	1 ENV_VILV	P35954 visna lenti
21	52.5	21.8	991	1 ENV_VILV2	P23423 visna lenti
22	52.5	21.8	1154	1 VGL2_IBVD2	P12722 avian lenti
23	52.5	21.8	1162	1 VGL2_IBVD	P11223 avian lenti
24	52.5	21.8	1162	1 VGL2_IBVD	P12650 avian lenti
25	52.5	21.8	1162	1 VGL2_IBVD	P12651 avian lenti
26	52.5	21.8	1163	1 VGL2_IBVD	P05135 avian lenti
27	52	21.6	68	1 Y121_BPT4	O02405 bacterioph
28	51.5	21.4	162	1 DSRB_NEIMA	O9jfc6 neisseria m
29	51.5	21.4	162	1 DSRB_NEIMA	O9jfc6 neisseria m
30	51.5	21.4	173	1 NUCG_ANASP	O44241 anabaena sp
31	51.5	21.4	443	1 FDCG_BRANA	P48627 brassica na
32	51.5	21.4	448	1 FDCG_ARATH	P46312 arabidopsis
33	51.5	21.4	989	1 ENV_VILV1	P23422 visna lenti

34	51.5	21.4	1262	1 MYO6_HUMAN	O9um54 homo sapien
35	51.5	21.4	1265	1 MYO6_MOUSE	O64331 mus musculu
36	51	21.2	126	1 YDQ3_MYCTU	O11013 mycobacteri
37	51	21.2	196	1 YAO5_SCHPO	O09677 schizosach
38	51	21.2	295	1 YDQ2_ECO57	O8x277 escherichia
39	51	21.2	295	1 YDQ2_ECO57	P76213 escherichia
40	51	21.2	556	1 MEND_ECOLI	P17109 e menaquin
41	51	21.2	2292	1 P04G_EMCVB	P17593 encephalomy
42	51	21.2	2292	1 P04G_EMCVD	P17594 encephalomy
43	50.5	21.0	293	1 YDQ2_SALTI	O82695 salmonella
44	50.5	21.0	293	1 YDQ2_SALTY	O82696 salmonella
45	50.5	21.0	469	1 GATR_THETH	O91cx2 thermus the

ALIGNMENTS

RESULT 1	ID	INDC_BOVIN	STANDARD:	PRT:	144 AA.
AC	P33046;				
DT	01-OCT-1993 (Rel. 27, Created)				
DT	01-OCT-1993 (Rel. 27, Last sequence update)				
DT	01-NOV-1997 (Rel. 35, Last annotation update)				
DE	Indolicidin precursor.				
OS	Bos taurus (bovine).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;				
OX	Bovidae; Bovinae; Bos.				
RN	NCBI_TaxID=9913;				
RP	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Bone marrow;				
RX	MEDLINE=92393368; PubMed=1520337;				
RA	del Sal G., Storici P., Schneider C., Romeo D., Zanetti M.;				
RT	"CDNA cloning of the neutrophil bactericidal peptide indolicidin.";				
RL	Biochem. Biophys. Res. Commun. 187:467-472(1992).				
RN	[2]				
RP	SEQUENCE OF 131-143.				
RC	TISSUE=Neutrophils;				
RX	MEDLINE=92165771; PubMed=1537821;				
RA	Selsted M.E., Novotny M.J., Morris W.L., Tang Y.-Q., Smith W.;				
RT	Cullor J.S.;				
RL	"Indolicidin, a novel bactericidal tridecapeptide amide from neutrophils.";				
RT	J. Biol. Chem. 267:4292-4295(1992).				
CC	-1- FUNCTION: POTENT MICROBICIDAL ACTIVITY, ACTIVE AGAINST STAPHYLOCOCCUS AUREUS AND ESCHERICHIA COLI.				
CC	-1- TISSUE SPECIFICITY: LARGE GRANULES OF NEUTROPHILS.				
CC	-1- PTM: ELASTASE MIGHT BE RESPONSIBLE FOR ITS MATURATION.				
CC	-1- SIMILARITY: BELONGS TO THE CATHELICIDIN FAMILY.				
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CC	EMBL: X67340; CAA47755.1; -				
DR	PIR: JCI222; JCI222.				
DR	PIR: A42387; A42387.				
DR	InterPro: IPR001894; Cathelicidin.				
DR	Pfam: PF00666; Cathelicidins; 1.				
DR	ProDom: PD001838; Cathelicidin; 1.				
DR	PROSITE: PS00946; CATHELICIDINS_1; 1.				
DR	PROSITE: PS00947; CATHELICIDINS_2; 1.				
KW	Antibiotic; Amidation; Signal.				
FT	SIGNAL	1	29		POTENTIAL.
FT	PROPEP	30	130		
FT	PEPTIDE	131	143		INDOLICIDIN.
FT	MOD_RES	30	30		PYRROLIDONE CARBOXYLIC ACID (BY

```

FT DISULFID 85 96 SIMILARITY).
FT DISULFID 107 124 BY SIMILARITY.
FT MOD_RES 143 143 AMIDATION (G-144 PROVIDE AMIDE GROUP).
SQ SEQUENCE 144 AA; 16479 MW; E3B1CBBE5C09911 CRC64;

Query Match 32.4%; Score 78; DB 1; Length 144;
Best Local Similarity 55.6%; Pred. No. 0.0049;
Matches 10; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 19 EAEPIMLKKWMPWRR 36
   I : : : : :
Db 126 ELQSVILPKNPMPWRR 143

RESULT 2
YMA3_BACST
ID YMA3_BACST STANDARD; PRT; 314 AA.
AC 045633;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 16-OCF-2001 (Rel. 40, Last annotation update)
OS Hypothetical 35.7 kDa protein in mala 3 region (ORF3).
OC Bacillus stearothermophilus.
OC Bacteria; Firmicutes; Bacillales; Geobacillus.
OX NCBI_TaxID=1422;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 7953;
RX MEDLINE=94247374; PubMed=8190087;
RA Liang E.C., Ferencik T.;
RT "Molecular cloning of a maltose transport gene from Bacillus
   stearothermophilus and its expression in Escherichia coli K-12.";
RL Mol. Gen. Genet. 243:343-352(1994).
CC -1- SIMILARITY: BELONGS TO THE UPF0097 FAMILY.
CC -----
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CC -----
DR EMBL: L13418; AAA1981.1; -
DR InterPro: IPR004175; 2.5_1lgase.
DR Pfam: PF02834; 2.5_1lgase; 2.
KW Hypothetical protein.
SQ SEQUENCE 314 AA; 35735 MW; B54E25FD3F72BFC4 CRC64;

Query Match 25.7%; Score 62; DB 1; Length 314;
Best Local Similarity 34.7%; Pred. No. 0.99;
Matches 17; Conservative 5; Mismatches 13; Indels 14; Gaps 3;

OY 2 LKKWPMWRKRHEAPEA-----EP-----IMLKKWMPW-----WRR 36
   I I I : : I I I : I I I : I I I
Db 222 LKQWQEDAKARWEARADGARREGETWDLDPKPSWERTLGRWR 270

RESULT 3
POLG_EMCV
ID POLG_EMCV STANDARD; PRT; 2290 AA.
AC P03304;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Genome polyprotein [Contains: Coat proteins VP1 TO VP4; Core proteins
   P2A TO P2C, P3A; Genome-linked protein VPg; Picornain 3C
   (EC 3.4.22.28) (Protease 3C) (P3C); RNA-directed RNA polymerase P3D
   (EC 2.7.7.48)].
DE Encephalomyocarditis virus.
OS Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Cardiovirus.

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OX NCBI_TaxID=12104;
RN 11
RP SEQUENCE FROM N.A.
RX MEDLINE=84169586; PubMed=6324136;
RA Palmenberg A.C., Kirby E.M., Janda M.R., Drake N.L., Duke G.M.,
   Polratz K.F., Collett M.S.;
RT "The nucleotide and deduced amino acid sequences of the
   encephalomyocarditis viral polyprotein coding region.";
RL Nucleic Acids Res. 12:2969-2985(1984).
CC -1- FUNCTION: P3C POLYPEPTIDE IS A PROTEASE THAT CLEAVES AT CERTAIN
   O/G SITES IN THE POLYPROTEIN. IT MAY BE A CYSTEINE PROTEASE.
CC -1- CATALYTIC ACTIVITY: Selective cleavage of Gln-1-gly bond in the
   poliovirus polyprotein. In other picornavirus reactions Glu may be
   substituted for Gln, and Ser or Thr for Gly.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
   (RNA)(N).
CC -1- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAEDRAL UNITS,
   EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,
   VP3, AND VP4.
CC -1- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
CC -1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C3.
CC -----
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CC -----
DR EMBL: X00463; CAA25152.1; -
DR PIR: A03906; GNNE.
DR HSSP: P12296; 2MEV.
DR MEROPS: C03.009; -.
DR InterPro: IPR000605; RNA_helicase.
DR InterPro: IPR001205; RNA_pol_P3D.
DR Pfam: PF00073; Htv; 3.
DR Pfam: PF00680; RNA_dep_RNA_pol; 1.
DR Pfam: PF00910; RNA_helicase; 1.
KW Polyprotein; Coat protein; Core protein; Transferase;
   RNA-directed RNA polymerase; Hydrolase; Thiol protease; Myristate.
FT CHAIN 1
FT PROPEP 1 67
FT CHAIN 68 136 COAT PROTEIN VP4 (RHO).
FT CHAIN 137 391 COAT PROTEIN VP2 (BETA).
FT CHAIN 392 622 COAT PROTEIN VP3 (GAMMA).
FT CHAIN 623 910 COAT PROTEIN VP1 (ALPHA).
FT CHAIN 911 1056 CORE PROTEIN P2A (G).
FT CHAIN 1057 1192 CORE PROTEIN P2B (I).
FT CHAIN 1193 1517 CORE PROTEIN P2C (F).
FT CHAIN 1518 1605 CORE PROTEIN P3A.
FT CHAIN 1606 1625 GENOME-LINKED PROTEIN VPg (H).
FT CHAIN 1626 1830 PICORNAIN 3C (P22).
FT CHAIN 1831 2290 RNA-DIRECTED RNA POLYMERASE P3D (E).
FT LIPID 68 MIRISTATE (BY SIMILARITY).
FT ACT_SITE 1784 1784 PROTEASE (POTENTIAL).
FT ACT_SITE 1802 1802 PROTEASE (POTENTIAL).
SQ SEQUENCE 2290 AA; 255756 MW; 26BC81BB7CF68CB5 CRC64;

Query Match 24.7%; Score 59.5; DB 1; Length 2290;
Best Local Similarity 26.2%; Pred. No. 14;
Matches 11; Conservative 6; Mismatches 8; Indels 17; Gaps 1;

OY 6 PMWPMWRKRHEAPEA-----MILKKW 30
   I I I : : I I I : : I I I
Db 967 PMWPMWRKRHEAPEA-----MILKKW 1008

RESULT 4
MMLA_STRCO
ID MMLA_STRCO STANDARD; PRT; 711 AA.
AC Q53902;
DT 30-MAY-2000 (Rel. 39, Created)

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DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DR Putative membrane protein actin-3
GN ACT11-3 OR SC05084 OR SCBAC2861.10.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91347376; PubMed=1878971;
RA Fernandez-Moreno M.A., Caballero J.L., Hopwood D.A., Malpartida F.;
RT "The act cluster contains regulatory and antibiotic export genes,
RT direct targets for translational control by the hlaA tRNA gene of
RT Streptomyces";
RL Cell 66:769-780(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=A3(2) / M145;
RC MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Taylor K.,
RA Warren T., Watzdorf A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2)";
RL Nature 417:141-147(2002).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (potential).
CC -1- SIMILARITY: BELONGS TO THE MRP FAMILY.
CC
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CC -----
DR EMBL: M64683; AAA26691.1; -.
DR EMBL: AL593842; CAC4197.1; -.
DR InterPro: IPR004707; Actin.
DR InterPro: IPR000731; HMGCR/patch_5TM.
DR Pfam: PF03176; MMP1. 2.
DR TIGRfam: TIGR00833; actin; 1.
DR PROSITE: PS50156; SSD. 2.
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 14 34
FT TRANSMEM 175 195
FT TRANSMEM 199 219
FT TRANSMEM 235 255
FT TRANSMEM 281 301
FT TRANSMEM 313 333
FT TRANSMEM 369 389
FT TRANSMEM 516 536
FT TRANSMEM 540 560
FT TRANSMEM 573 593
FT TRANSMEM 623 643
FT TRANSMEM 645 665
FT TRANSMEM 711 AA; 74862 MW; A5466BDBABED1B6 CRC64;
SQ

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Query Match 23.7%; Score 57; DB 1; Length 711;
Best Local Similarity 47.4%; Pred. No. 9.1;
Matches 9; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
DB 332 IFGRVFWFAPRKHGTEPD 350

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RESULT 5
ID ATP8_ANAPL STANDARD; PRT; 55 AA.
AC P50655;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE ATP synthase protein 8 (EC 3.6.3.14) (ATPase subunit 8) (a6L).
GN ATP8 OR ATP8.
OS Anas platyrhynchos (Domestic duck).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
OX NCBI_TaxID=8839;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=pekin breed; TISSUE=Liver;
RC MEDLINE=94047124; PubMed=8230253;
RA Ramirez V., Savole P., Morais R.;
RT "Molecular characterization and evolution of a duck mitochondrial
RT genome";
RL J. Mol. Evol. 37:296-310(1993).
CC -1- FUNCTION: THIS IS ONE OF THE CHAINS OF THE NONENZYMATIC COMPONENT
CC (CF0) SUBUNIT OF THE MITOCHONDRIAL ATPASE COMPLEX.
CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(in) = ADP + phosphate +
CC H(+)(out).
CC -1- SUBCELLULAR LOCATION: Membrane-bound.
CC -1- SIMILARITY: BELONGS TO THE ATPASE PROTEIN 8 FAMILY.
CC
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CC -----
DR EMBL: L22476; AAA12037.1; -.
DR InterPro: IPR001421; ATPase8_mit.
DR Pfam: PF00895; ATP-synt_8; 1.
KW Hydrogen ion transport; CF(0); Mitochondrion; Transmembrane.
FT TRANSMEM 8 24
FT TRANSMEM 55 AA; 6334 MW; 41284BAB1525B99 CRC64;
SQ

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```

Query Match 23.0%; Score 55.5; DB 1; Length 55;
Best Local Similarity 50.0%; Pred. No. 1.1;
Matches 9; Conservative 2; Mismatches 6; Indels 1; Gaps 1;
DB 18 PEAEPIMLKKPW-WPW 34
DB 37 PSKKPSLITKPTWMPW 54

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RESULT 6
ID ENV_CAEGV STANDARD; PRT; 942 AA.
AC P31627;
DT 01-JUL-1993 (Rel. 26, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Env polyprotein precursor (Coat polypeptide) [Contains: Surface
DE protein; Transmembrane protein].
DE ENV.
GN
OS Caprine arthritis encephalitis virus (strain 663) (CAEV).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11662;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 81-95.
RX MEDLINE=92015464; PubMed=1656067;
RA Knowles D.P., Jr., Cheevers W.P., McGuire T.C., Brassfield A.L.,
RA Harwood W.G., Stem T.A.;

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RT "Structure and genetic variability of envelope glycoproteins of two
RT antigenic variants of caprine arthritis-encephalitis lentivirus.";
RT J. Virol. 65:5744-5750(1991).
[2]
RN REVISIONS.
RA Knowles D.P.;
RL Submitted (Apr-2000) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL, M60855; AA88709.2; -.
DR PIR, A41307; VCLJC6.
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
KW Glycoprotein; Coat protein; Polypeptide; Transmembrane.
FT PEPTIDE 1 80
FT CHAIN 1 630
FT CHAIN 1 630
FT DOMAIN 1 630
FT TRANSMEM 631 659
FT DOMAIN 660 820
FT TRANSMEM 821 942
FT DOMAIN 942 942
FT CARBOHYD 51 51
FT CARBOHYD 98 98
FT CARBOHYD 131 131
FT CARBOHYD 176 176
FT CARBOHYD 228 228
FT CARBOHYD 331 331
FT CARBOHYD 348 348
FT CARBOHYD 354 354
FT CARBOHYD 370 370
FT CARBOHYD 379 379
FT CARBOHYD 400 400
FT CARBOHYD 404 404
FT CARBOHYD 435 435
FT CARBOHYD 441 441
FT CARBOHYD 447 447
FT CARBOHYD 457 457
FT CARBOHYD 467 467
FT CARBOHYD 481 481
FT CARBOHYD 493 493
FT CARBOHYD 503 503
FT CARBOHYD 509 509
FT CARBOHYD 527 527
FT CARBOHYD 534 534
SQ SEQUENCE 942 AA; 108437 MW; 5B0E1F0F3D355FAA CRC64;

Query Match 23.0%; Score 55.5; DB 1; Length 942;
Best Local Similarity 21.4%; Pred. No. 18;
Matches 15; Conservative 7; Mismatches 9; Indels 39; Gaps 4;

OY 3 KKWPW-----WP-----WRKKHAEPEAF-----PIMI 25
DB 143 EWWPNNTYHWPLMOMENVRWIKENIAENKKRKNSTKGIEELLAGTIRGRCPVYPFAL 202
OY 26 LK--KWPMP 33
DB 203 LKCTKWCWYP 212

DR 01-JUN-1994 (Rel. 29, Last annotation update)
DE ENV polypeptide precursor (Coat polypeptide).
GN ENV
OS Ovine lentivirus (strain SA-OMV).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11664;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90223989; PubMed=2158181;
RA Querat G., Autouly G., Sonigo P., Vigne R.;
RT "Nucleotide sequence analysis of SA-OMV, a virus-related ovine
RT lentivirus: phylogenetic history of lentiviruses";
RL Virology 175:434-447(1990).
CC -----
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CC -----
DR EMBL, M34193; AAA46783.1; -.
DR EMBL, M31646; AAA66817.1; -.
DR PIR, G46335; G46335.
DR HIV; M34193; ENVSOMVSACG.
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
KW Glycoprotein; Coat protein; Polypeptide; Transmembrane.
FT PEPTIDE 1 101
FT CHAIN 102 662
FT CHAIN 663 990
FT TRANSMEM 842 863
FT CARBOHYD 141 141
FT CARBOHYD 162 162
FT CARBOHYD 207 207
FT CARBOHYD 259 259
FT CARBOHYD 299 299
FT CARBOHYD 363 363
FT CARBOHYD 386 386
FT CARBOHYD 402 402
FT CARBOHYD 413 413
FT CARBOHYD 434 434
FT CARBOHYD 438 438
FT CARBOHYD 469 469
FT CARBOHYD 474 474
FT CARBOHYD 480 480
FT CARBOHYD 490 490
FT CARBOHYD 500 500
FT CARBOHYD 514 514
FT CARBOHYD 526 526
FT CARBOHYD 536 536
FT CARBOHYD 542 542
FT CARBOHYD 550 550
FT CARBOHYD 560 560
FT CARBOHYD 567 567
FT CARBOHYD 703 703
FT CARBOHYD 771 771
FT CARBOHYD 778 778
FT CARBOHYD 794 794
SQ SEQUENCE 990 AA; 114498 MW; 279B816B55614F3 CRC64;

Query Match 23.0%; Score 55.5; DB 1; Length 990;
Best Local Similarity 20.0%; Pred. No. 19;
Matches 14; Conservative 9; Mismatches 8; Indels 39; Gaps 4;

OY 3 KKWPW-----WP-----WRKKHAEPEAF-----PIMI 25
DB 174 QEWPNNTYHWPLMOMENVRWIKENIAENKKRKNSTKGIEELLAGTIRGRCPVYPFAL 233
OY 26 LK--KWPMP 33
DB 234 LKCEWMCWYP 243

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RESULT 8
ID YD55_MYCTU STANDARD; PRT; 715 AA.
AC 011025;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein RV1355C.
GN RV1355C OR MT1398 OR MTCY02B10.19C.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltham T., Gentles S., Hamlin N., Holtroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrett B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence."
RL Nature 393:537-544(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains."
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
DR EMBL: 275555; CAA99988.1; -
DR EMBL: AE007012; AAK45661.1; ALT_INIT.
DR TIGR: MT1398; -
DR TubercuList: RV1355C; -
DR InterPro: IPR000594; Thif_domain.
DR Pfam: PF00899; Thif; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 715 AA; 78181 MW; 455495248A56041C CRC64;

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Query Match 22.8%; Score 55; DB 1; Length 715;
Best Local Similarity 38.1%; Pred. No. 16;
Matches 8; Conservative 7; Mismatches 4; Indels 2; Gaps 1;

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OY 18 PEAPEIMI--LKKPMPMPMR 36
ID 53 PDPDPDLEAKRWAYPMWR 73

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RESULT 9
AP22_APIME STANDARD; PRT; 144 AA.
ID AP22_APIME STANDARD; PRT; 144 AA.
AC P35361; P11525; P11526;
DT 01-OCT-1989 (Rel. 12, Created)

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DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Apidaecin precursor, type 22.
OS Apis mellifera (Honeybee).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
OC Aculeata; Apoidea; Apidae; Apis.
OX NCBI_TaxID=7460;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93223697; PubMed=8467807;
RA Casteels P., Capaci T., Casteels P., Tempet P.;
RT "Apidaecin multipetide precursor structure: a putative mechanism for
RT amplification of the insect antibacterial response."
RL EMBO J. 12:1569-1578(1993).
RN [2]
RP SEQUENCE (APIDACIN IA/IB).
RC TISSUE=Hemolymph;
RX MEDLINE=90005446; PubMed=2676519;
RA Casteels P., Ampe C., Jacobs F., Vaek M., Tempet P.;
RT "Apidaecins: antibacterial peptides from honeybees."
RL EMBO J. 8:2387-2391(1989).
CC -1- FUNCTION: APIDACIN HAVE BACTERICIDAL ACTIVITY; PREDOMINANTLY
CC AGAINST GRAM-NEGATIVE BACTERIA. THEY SEEM TO INTERFERE WITH CELL
CC PROPAGATION.
CC -----
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CC -----
DR EMBL: X72576; CAA51168.1; -
DR PIR: S05383; S05383.
DR PIR: S06675; S06675.
DR PIR: S35331; S35331.
DR InterPro: IPR004828; Apidaecin.
DR Pfam: PF00807; Apidaecin; 4.
KW Insect immunity; Antibiotic; Hemolymph; Signal; Multigene family;
KW Cleavage on pair of basic residues; Repeat.
FT SIGNAL 1 19 POTENTIAL.
FT PROPEP 35 42
FT PEPTIDE 43 60 APIDACIN IB.
FT PROPEP 63 70
FT PEPTIDE 71 88 APIDACIN IB.
FT PROPEP 91 98
FT PEPTIDE 99 116 APIDACIN IB.
FT PROPEP 119 126
FT PEPTIDE 127 144
SQ SEQUENCE 144 AA; 16539 MW; 6FA1AD74CB77108D CRC64;

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Query Match 22.4%; Score 54; DB 1; Length 144;
Best Local Similarity 64.7%; Pred. No. 4;
Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

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OY 6 PMWPMRRKHEAPPAEP 22
ID 26 PTRPTRLRREAEPAEP 42

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RESULT 10
SYCL_MYCTU STANDARD; PRT; 469 AA.
ID SYCL_MYCTU STANDARD; PRT; 469 AA.
AC P96862;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cysteiny1-tRNA synthetase I (EC 6.1.1.16) (Cysteine--tRNA ligase 1)
DE (CysRS 1).
GN CYSS1 OR CYSS OR RV3580C OR MT3686 OR MTCY06G11.27C.
OS Mycobacterium tuberculosis.

```


DE E2 glycoprotein precursor (Spike glycoprotein) (Peplomer protein).
GN S.
OS Human coronavirus (strain 229E).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxId=11137;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90264837; PubMed=2345367;
RA Raabe T., Scheile-Prinz B., Siddell S.G.;
RT "Nucleotide sequence of the gene encoding the spike glycoprotein of
RT human coronavirus HCV 229E.";
RL J. Gen. Virol. 71:1065-1073(1990).
CC -I- FUNCTION: THE PEPLIMER PROTEIN MEDIATES THE BINDING OF VIRIONS
CC TO THE HOST CELL RECEPTOR AND IS INVOLVED IN MEMBRANE FUSION
CC AND IN STINGYUM FORMATION.
CC -I- SUBCELLULAR LOCATION: Type I membrane protein.
CC -----
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CC -----
DR EMBL: X16816; CAA34723.1; -
DR PIR: A34766; VGIHHC.
DR InterPro: IPR002551; Corona_S1.
DR InterPro: IPR002552; Corona_S2.
DR Pfam: PF01600; Corona_S1; 1.
DR Pfam: PF01601; Corona_S2; 1.
KM Glycoprotein; Envelope protein; Transmembrane; Signal.
FT SIGNAL 1 15
FT CHAIN 16 1173
FT DOMAIN 16 1115
FT TRANSMEM 1116 1135
FT DOMAIN 1136 1173
FT DOMAIN 1136 1157
FT CARBOHYD 23 23
FT CARBOHYD 62 62
FT CARBOHYD 98 98
FT CARBOHYD 147 147
FT CARBOHYD 171 171
FT CARBOHYD 176 176
FT CARBOHYD 220 220
FT CARBOHYD 243 243
FT CARBOHYD 326 326
FT CARBOHYD 333 333
FT CARBOHYD 440 440
FT CARBOHYD 464 464
FT CARBOHYD 518 518
FT CARBOHYD 538 538
FT CARBOHYD 542 542
FT CARBOHYD 568 568
FT CARBOHYD 581 581
FT CARBOHYD 587 587
FT CARBOHYD 663 663
FT CARBOHYD 671 671
FT CARBOHYD 930 930
FT CARBOHYD 1015 1015
FT CARBOHYD 1020 1020
FT CARBOHYD 1037 1037
FT CARBOHYD 1049 1049
FT CARBOHYD 1061 1061
FT CARBOHYD 1066 1066
FT CARBOHYD 1076 1076
FT CARBOHYD 1082 1082
FT CARBOHYD 1096 1096
SQ SEQUENCE 1173 AA; 128639 MW; B9CA9A41A796B3BD CRC64;
Query Match 22.4%; Score 54; DB 1; Length 1173;
Best Local Similarity 85.7%; Pred. No. 35;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 4 KMFMPW 10
Db 1113 KMFMPW 1119
RESULT 13
ID CORI_HUMAN STANDARD; PRT; 1042 AA.
AC Q9Y505; Q9YH2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Atrial natriuretic peptide-converting enzyme (EC 3.4.21.-) (pro-ANP-
DE converting enzyme) (Corin) (Heart specific serine proteinase ATC2).
GN CRN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Heart;
RX MEDLINE=99262646; PubMed=10329693;
RA "Corin, a mosaic transmembrane serine protease encoded by a novel cDNA
RA from human heart.";
RL J. Biol. Chem. 274:14926-14935(1999).
RN [2]
RP SEQUENCE OF 734-1040 FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=20534769; PubMed=11082206;
RA Hooper J.D., Scaram A.L., Clarke B.E., Normyle J.F., Antalis T.M.;
RT "Localization of the mosaic transmembrane serine protease corin to
RT heart myocytes.";
RL Eur. J. Biochem. 267:6931-6937(2000).
RN [3]
RP CHARACTERIZATION.
RX MEDLINE=20539740; PubMed=10880574;
RA Yan W., Wu F., Morser J., Wu Q.;
RT "Corin, a transmembrane cardiac serine protease, acts as a pro-atrial
RT natriuretic peptide-converting enzyme.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:8525-8529(2000).
CC -I- FUNCTION: CONVERTS PRO-ANP TO ANP. CLEAVES PRO-ANP SPECIFICALLY
CC BETWEEN ARG-123 AND SER-124.
CC -I- SUBCELLULAR LOCATION: Type II membrane protein.
CC -I- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART. EXPRESSED IN HEART
CC MYOCYTES.
CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -I- SIMILARITY: CONTAINS 7 LDL-RECEPTOR CLASS A DOMAINS.
CC -I- SIMILARITY: CONTAINS 2 FRIZZLED (FZ) DOMAINS.
CC -I- SIMILARITY: CONTAINS 1 SRCR DOMAIN.
CC -----
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CC -----
DR EMBL: AF13845; AAD31850.1; -
DR EMBL: AF113248; AAF21966.1; -
DR HSSP: P00763; IDPO.
DR MEROPS: S01.019; -
DR MIM: 605236; -
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000024; Fz_domain.
DR InterPro: IPR001217; LDL_recept_A.
DR InterPro: IPR001254; Ser_protease_Try.
DR InterPro: IPR001190; Srcr_receptor.
DR Pfam: PF00057; Idl_recept_a; 6.


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FT DOMAIN 373 408 IDL-RECEPTOR CLASS A 2.
FT DOMAIN 409 445 IDL-RECEPTOR CLASS A 3.
FT DOMAIN 446 483 IDL-RECEPTOR CLASS A 4.
FT DOMAIN 518 641 F2.
FT DOMAIN 647 682 IDL-RECEPTOR CLASS A 5.
FT DOMAIN 683 721 IDL-RECEPTOR CLASS A 6.
FT DOMAIN 722 757 IDL-RECEPTOR CLASS A 7.
FT DOMAIN 758 853 SRCR.
FT DOMAIN 869 1113 SERINE PROTEASE.
FT ACT_SITE 910 910 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 959 959 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 1052 1052 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 857 979 BY SIMILARITY.
FT DISULFID 895 911 BY SIMILARITY.
FT DISULFID 1022 1037 BY SIMILARITY.
FT DISULFID 1048 1077 BY SIMILARITY.
FT CARBOHYD 147 147 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 202 202 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 208 208 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 298 298 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 317 317 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 373 373 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 411 411 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 444 444 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 481 481 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 519 519 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 537 537 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 635 635 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 719 719 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 765 765 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 828 828 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 970 970 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1089 1089 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 1113 AA: 122984 MW: 845525CF20DD8EC CRC64;

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Query Match 22.2%; Score 53.5; DB 1; Length 1113;
Best Local Similarity 36.0%; Pred. No. 38;
Matches 9; Conservative 5; Mismatches 8; Indels 3; Gaps 1;

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QY 8 WPMRRKHEAPEAE--PIMILKKW 29
      111:  ::11  ::1111
Db 880 WPMCSLQSEPSGICGCVLIARW 904

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RESULT 15
FDCG_SQYBN STANDARD; PRT; 424 AA.
AC P48628;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Omega-6 fatty acid desaturase, chloroplast precursor (EC 1.14.99.-).
OS Glycine max (soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Seed;
RX MEDLINE=94345008; PubMed=8066133;
RA Hitz W.D., Carlson T.J., Booth J.R. Jr., Kinney A.J., Stecca K.L.,
RA Yadev N.S.;
RT "Cloning of a higher-plant plastid omega-6 fatty acid desaturase cDNA
RT and its expression in a cyanobacterium.";
RL Plant Physiol. 105:635-641(1994).
CC -1- FUNCTION: CHLOROPLAST OMEGA-6 FATTY ACID DESATURASE INTRODUCES
CC THE SECOND DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
CC ACIDS. IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
CC TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
CC -1- PATHWAY: Polyunsaturated fatty acid biosynthesis.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).

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CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
CC -----
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CC -----
CC EMBL: I29215; AAA50158.1; -
CC InterPro: IPR001225; FA_desaturase.
CC Pfam: PF00487; FA_desaturase.1.
CC ProDom: PD001081; FA_desaturase.1.
CC Oxidoreductase; Fatty acid biosynthesis; Chloroplast; Membrane;
CC Transf. 1
CC TRANSIT 1 63 CHLOROPLAST (BY SIMILARITY).
CC CHAIN 64 424 OMEGA-6 FATTY ACID DESATURASE.
CC DOMAIN 165 169 HISTIDINE BOX-1.
CC FT DOMAIN 201 205 HISTIDINE BOX-2.
CC FT DOMAIN 361 365 HISTIDINE BOX-3.
SQ SEQUENCE 424 AA: 49641 MW: 4F3DF524B1A2009 CRC64;

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Query Match 22.0%; Score 53; DB 1; Length 424;
Best Local Similarity 34.4%; Pred. No. 17;
Matches 11; Conservative 7; Mismatches 12; Indels 2; Gaps 2;

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QY 5 WPMWPMRRKHEAPEAEPIIMILKKWMPMP-WR 35
      11: 111111 1: 1: 1: 1: 1:
Db 192 YPEPMPFKHNRH-HAKTNLRLREDTAMHPYWK 222

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Search completed: December 11, 2002, 15:39:03
Job time : 13 secs

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OM protein - protein search, using sw model

Run on: December 11, 2002, 15:38:09 ; Search time 19 seconds
(without alignments)
187.209 Million cell updates/sec

Title: US-09-444-281-35-27-35
Perfect score: 241
Sequence: 1 ILKKWPMWPMWRKHEAPEADPEMILKKWPMWPMWRK 37

Scoring table: BLOSUM62
Gapop 10.0 , Gapept 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	78	32.4	144	1 JCI222	indolicidin precursor
2	63	26.1	192	2 H86543	hypothetical prote
3	63	26.1	192	2 D72081	conserved hypothet
4	62	25.7	314	2 S43916	hypothetical prote
5	60	24.9	381	2 B87470	hypothetical prote
6	59.5	24.7	114	2 T36208	hypothetical prote
7	59.5	24.7	2280	1 GNNYE	hypothetical prote
8	59	24.5	95	2 E86447	genome polyprotein
9	59	24.5	485	2 S74708	protein F5D14.5 [1
10	58	24.1	107	2 T35634	hypothetical prote
11	58	24.1	513	2 S21976	hypothetical prote
12	57.5	23.9	376	2 T40591	probable RNA-direc
13	57	23.7	711	2 C40046	hypothetical prote
14	56	23.2	452	2 T28094	antibiotic transpo
15	55.5	23.0	527	2 S33068	hypothetical prote
16	55.5	23.0	990	1 G46335	myosin heavy chain
17	55.5	23.0	1940	2 A59287	env polyprotein pr
18	55	22.8	245	2 C69459	myosin heavy chain
19	55	22.8	352	2 S77448	transcription regu
20	55	22.8	715	2 B70741	hypothetical prote
21	54.5	22.6	134	2 E72532	probable moey prot
22	54.5	22.6	340	2 PH0217	hypothetical prote
23	54.5	22.6	451	2 S30401	reverse transcript
24	54.5	22.6	547	2 S74535	hypothetical prote
25	54	22.4	144	2 S35331	hypothetical prote
26	54	22.4	187	2 AB1647	apidecin 22 precu
27	54	22.4	469	2 B70607	hypothetical prote
28	54	22.4	473	2 C86949	probable cysteiny
29	54	22.4	1173	1 VGIHHC	E2 glycoprotein pr

30	53.5	22.2	538	2 B84759	hypothetical prote
31	53.5	22.2	1113	2 JE0315	low-density lipopr
32	53	22.0	68	2 E82799	hypothetical prote
33	53	22.0	406	2 H69143	coenzyme P420-redu
34	53	22.0	424	2 T07742	omega-6 desaturase
35	53	22.0	480	2 JC7552	Shb-1like adapter p
36	53	22.0	691	2 D71430	hypothetical prote
37	53	22.0	949	2 E75352	glycine cleavage s
38	53	22.0	2292	2 S35961	capsid polyprotein
39	52.5	21.8	55	2 T11026	H+-transporting tw
40	52.5	21.8	228	2 AD3326	chloramphenicol O-
41	52.5	21.8	449	2 C84618	hypothetical prote
42	52.5	21.8	471	2 T50016	transcription fact
43	52.5	21.8	490	2 T21365	hypothetical prote
44	52.5	21.8	518	2 T29589	hypothetical prote
45	52.5	21.8	621	2 S37664	peptidomeric polypro

ALIGNMENTS

RESULT 1
JCI222
indolicidin precursor - bovine
N:Alternate names: antimicrobial peptide
C:Species: Bos primigenius taurus (cattle)
C>Date: 10-Sep-1999 #sequence, revision 10-Sep-1999 #text, change 10-Sep-1999
C:Accession: JCI222; A42387; S25664
R:del Sal, G.; Storici, P.; Schneider, C.; Romeo, D.; Zanetti, M.
Biochem. Biophys. Res. Commun. 187, 467-472, 1992
A:Title: CDNA cloning of the neutrophil bactericidal peptide indolicidin.
A:Reference number: JCI222; MUID:92392368; PMID:1520337
A:Accession: JCI222
A:Molecule type: mRNA
A:Residues: 1-144 <SAL>
A:Cross-references: EMBL:X67340; NID:9462; PIDN:CAA47755.1; PID:9463
A:Experimental source: bone marrow
R:Selsted, M.E.; Novotny, M.J.; Morris, W.L.; Tang, Y.Q.; Smith, W.; Cullor, J.S.
J. Biol. Chem. 267, 4292-4295, 1992
A:Title: Indolicidin, a novel bactericidal tridecapeptide amide from neutrophils.
A:Reference number: A42387; MUID:92165771; PMID:1537821
A:Accession: A42387
A:Molecule type: protein
A:Residues: 131-143 <SEL>
A:Experimental source: neutrophils
A:Note: sequence extracted from NCBI backbone (NCBIP:83840)
C:Superfamily: cathelin; cystatin homology
C:Keywords: amidated carboxyl end
F:1-29/Domain: signal sequence #status predicted <SIG>
F:32-129/Domain: cystatin homology <CYS>
F:30-110/Domain: propeptide #status predicted <PRO>
F:131-143/Product: indolicidin #status experimental <MAT>
F:143/Modified site: amidated carboxyl end (Arg) (amide in mature form from following

Query Match 32.4% Score 78; DB 1; Length 144;
Best local Similarity 55.6% Pred. No. 0.011;
Matches 10; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 19 EAEPIMLKKWPMWR 36
Db 126 ELQSVILPMKKWPMWR 143

RESULT 2
H86543
hypothetical protein CP10426 (imported) - Chlamydomonas pneumoniae (strain J138)
C:Species: Chlamydomonas pneumoniae, Chlamydia pneumoniae
C>Date: 02-Mar-2001 #sequence, revision 02-Mar-2001 #text, change 02-Mar-2001
C:Accession: H86543
R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.;
Nucleic Acids Res. 28, 2311-2314, 2000
A:Title: Comparison of whole genome sequences of Chlamydia pneumoniae J138.
A:Reference number: AB6491; MUID:20330349; PMID:10871362

C>Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 16-Jul-1999
 C/Accession: A03906; JN0383
 R:Palmenberg, A.C.; Kirby, E.M.; Janda, M.R.; Drake, N.L.; Duke, G.M.; Potratz, K.F.; Co
 Nucleic Acids Res. 12, 2969-2985, 1984
 A>Title: The nucleotide and deduced amino acid sequences of the encephalomyocarditis vir
 A:Reference number: A03906; M0ID:84169586; PMID:6524136
 A:Accession: A03906
 A:Molecule type: genomic RNA
 A:Residues: 1-2290 <PAL>
 A:Cross-references: GB:X00463; NID:961034; PIDN:CAA25152.1; PID:961035
 R:Belkov, N.A.; Chizhikov, V.E.; Blinov, V.M.; Katglov, V.A.; Mkrtyukov, N.N.; Gutorov,
 Bioray. Khim. 10, 274-279, 1994
 A>Title: Nucleotide sequence of the 3'-terminus of encephalomyocarditis virus RNA.
 A:Reference number: JN0383; M0ID:85022788; PMID:6091680
 A:Accession: JN0383
 A:Molecule type: genomic RNA
 A:Residues: 1337-1386, 'L', 1396-1517, 'A', 1519-1536, 'E', 1538-1556, 'S', 1558-1611, 'T', 1613-1
 A:Cross-references: GB:M54935
 A>Note: the authors translated the codon CAU for residue 713 as Thr and AAC for residue
 C:Superfamily: foot-and-mouth disease virus genome polypeptide
 C:Keywords: coat protein; core protein; genome-linked protein; hydrolase; nucleotidyltra
 F:1-67/Domain: leader peptide #status predicted <LDP>
 F:68-136/Product: coat protein VP4 #status predicted <VP4>
 F:137-391/Product: coat protein VP2 #status predicted <VP2>
 F:392-622/Product: coat protein VP3 #status predicted <VP3>
 F:623-910/Product: coat protein VP1 #status predicted <VP1>
 F:911-1056/Product: core protein P2-A #status predicted <P2A>
 F:1057-1192/Product: core protein P2-B #status predicted <P2B>
 F:1193-1517/Product: core protein P2-C #status predicted <P2C>
 F:1518-1605/Product: core protein P3-A #status predicted <P3A>
 F:1606-1625/Product: genome-linked protein VPg #status predicted <VPg>
 F:1626-1830/Product: proteinase #status predicted <PRTS>
 F:1831-2290/Product: RNA-directed RNA polymerase #status predicted <RDP>

Query Match 24.7%; Score 59.5; DB 1; Length 2290;
 Best Local Similarity 26.2%; Pred. No. 38;
 Matches 11; Conservative 6; Mismatches 8; Indels 17; Gaps 1;

QY 6 PMWPMRKHEAPEAPPI-----MLKKWP 30
 Db 967 PMWPMRKNTQAVLRAPCRVTMDIYKKRVRPRLPLVQKEMP 1008

RESULT 8
 E86447
 protein FSD14.5 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 C/Accession: E86447
 R:Rheologis, A.; Eckert, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 ansen, N.F.; Hughes, B.; Huizier, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maitl, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; M0ID:21016719; PMID:11130712
 A:Accession: E86447
 A:Molecule type: preliminary
 A>Status: preliminary
 A:Residues: 1-95 <SMO>
 A:Cross-references: GB:AE005172; NID:98920603; PIDN:AAF81325.1; GSPDB:GN00141
 C:Genetics:
 A:Gene: FSD14.5
 A:Map position: 1

Query Match 24.5%; Score 59; DB 2; Length 95;
 Best Local Similarity 21.3%; Pred. No. 1.6;
 Matches 10; Conservative 5; Mismatches 4; Indels 28; Gaps 3;

QY 5 WP-----WPMRKRKHEAPEAPPIMLK----KWPMPW 34
 Db 46 WPMVWVAVGAGGGRMMW-----PVLITVGGEMSMW 81

RESULT 9
 S74708
 hypothetical protein slr1306 - Synechocystis sp. (strain PCC 6803)
 C:Species: Synechocystis sp.
 A:Variety: PCC 6803
 C>Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
 C/Accession: S74708
 R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima,
 O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas
 DNA Res. 3, 109-136, 1996
 A>Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocys
 s.
 A:Reference number: S74322; M0ID:97061201; PMID:8905231
 A:Accession: S74708
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-485 <KAN>
 A:Cross-references: EMBL:D90901; GB:AB001339; NID:9151897; PIDN:BA016859.1; PID:d101
 A>Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 24.5%; Score 59; DB 2; Length 485;
 Best Local Similarity 29.3%; Pred. No. 8.6;
 Matches 12; Conservative 6; Mismatches 5; Indels 18; Gaps 2;

QY 6 PW-----WPMRKRKHEAPEAPPIW---ILKK 28
 Db 41 PMDQWGLMALSGGLVIMRMRRRRHAPPEQKQMLTREVLR 81

RESULT 10
 T35634
 hypothetical protein SC6G9.38 - Streptomyces coelicolor
 C:Species: Streptomyces coelicolor
 C>Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
 C/Accession: T35634
 R:Seeger, K.D.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A
 submitted to the EMBL Data Library, June 1999
 A:Reference number: 221584
 A:Accession: T35634
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-107 <SE>
 A:Cross-references: EMBL:AL079356; PIDN:CA845629.1; GSPDB:GN00070; SCOEDB:SC6G9.38
 A:Experimental source: strain A3(2)
 C:Genetics:
 A:Gene: SCOEDB:SC6G9.38

Query Match 24.1%; Score 58; DB 2; Length 107;
 Best Local Similarity 50.0%; Pred. No. 2.3;
 Matches 10; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 3 KKMPMPMKRKHAEPEAP 22
 Db 79 KKMPMSKRPERSAEPDAP 98

RESULT 11
 S21976
 probable RNA-directed DNA polymerase (EC 2.7.7.49) (clone MH2C) - rat retrotransposon
 N:Alternate names: reverse transcriptase
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 19-Mar-1997 #sequence_revision 17-Oct-1997 #text_change 26-Aug-1999
 C/Accession: S21976
 R:Kahre, O.; Ilves, H.; Speck, M.
 submitted to the EMBL Data Library, August 1991
 A:Reference number: S16783
 A:Accession: S21976
 A:Molecule type: mRNA

A:Residues: 1-513 <KAH>
 A:Cross-references: EMBL:X61295; NID:956521; PIDN:CAA43593.1; PID:956522
 A:Experimental source: clone M12C
 C:Genetics:
 A:Mobile element: retrotransposon L1
 C:Superfamily: pol polyprotein
 C:Keywords: nucleotidyltransferase; polypeptide; reverse transcriptase

Query Match 24.1%; Score 58; DB 2; Length 513;
 Best Local Similarity 39.4%; Pred. No. 12;
 Matches 13; Conservative 4; Mismatches 12; Indels 4; Gaps 2;

QY 1 ILKKWPMWPMR---RRHEAPEAPEIMILK-KW 29
 DB 373 IFSKMCMFMRATCRMOIDPCLSLCTKLKSKW 405

RESULT 12

T40591
 hypothetical protein SPBC646.15c - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 04-Mar-2000
 C:Accession: T40591
 R:Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
 submitted to the EMBL Data Library, January 1999
 A:Reference number: Z21938
 A:Accession: T40591
 A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
 A:Residues: 1-376 <SEE>
 A:Cross-references: EMBL:AL035216; PIDN:CAA22819.1; GSPDB:GN00067; SPDB:SPBC646.15c
 A:Experimental source: strain 972h-; cosmid c646
 C:Genetics:
 A:Gene: SPDB:SPBC646.15c
 A:Map position: 2
 A:Insertions: 48/1, 126/2, 312/2, 350/1
 C:Superfamily: Schizosaccharomyces pombe hypothetical protein SPBC646.15c

Query Match 23.9%; Score 57.5; DB 2; Length 376;
 Best Local Similarity 37.0%; Pred. No. 10;
 Matches 10; Conservative 3; Mismatches 7; Indels 7; Gaps 1;

QY 8 WPMRRKHEAPEAPEIMILKKWPMW 34
 DB 236 WHMKRKOKSSS-----LKYRPMGPM 255

RESULT 13

CA0046
 antibiotic transport-associated protein actr-3 - Streptomyces coelicolor
 C:Species: Streptomyces coelicolor
 C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 22-Oct-1999
 C:Accession: CA0046
 R:Fernandez-Moreno, M.A.; Caballero, J.L.; Hopwood, D.A.; Malpartida, F.
 Cell 66, 769-780, 1991
 A:Title: The act cluster contains regulatory and antibiotic export genes, direct targets
 A:Reference number: A40046; MUID:91347376; PMID:1878971
 A:Accession: CA0046
 A:Molecule type: DNA
 A:Residues: 1-711 <PER>
 A:Cross-references: GB:M64683; NID:9153143; PIDN:AAA26691.1; PID:9153146

Query Match 23.7%; Score 57; DB 2; Length 711;
 Best Local Similarity 47.4%; Pred. No. 23;
 Matches 9; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 ILKKWPMWPMRKRHEAPE 19
 DB 332 IFGRWFWPARPKHGTBD 350

RESULT 14
 T28094

hypothetical protein ZK899.2 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
 C:Accession: T28094
 R:Kershaw, J.
 submitted to the EMBL Data Library, September 1994
 A:Reference number: Z20468
 A:Accession: T28094
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-452 <MTL>
 A:Cross-references: EMBL:Z37140; PIDN:CAA85502.1; GSPDB:GN00028; CESP:ZK899.2
 A:Experimental source: clone ZK899
 C:Genetics:
 A:Gene: CESP:ZK899.2
 A:Map position: X
 A:Insertions: 34/3; 143/2; 227/2; 262/3; 380/3
 C:Superfamily: Caenorhabditis elegans hypothetical protein ZK899.2

Query Match 23.2%; Score 56; DB 2; Length 452;
 Best Local Similarity 32.3%; Pred. No. 19;
 Matches 10; Conservative 3; Mismatches 10; Indels 8; Gaps 2;

QY 4 KPMWPMRKRHEAPEAPEIMILKKWPMW 34
 DB 172 KLVWMTW---HDTDPN-----IFDRMNVPM 194

RESULT 15

S33068
 myosin heavy chain - fluke (Schistosoma mansoni) (fragment)
 N:Alternate names: surface antigen, 200K
 C:Species: Schistosoma mansoni
 C:Date: 22-Nov-1993 #sequence_revision 06-Sep-1996 #text_change 13-Feb-1998
 C:Accession: S33068
 R:Solomon, L.M.A.; Masterson, C.P.; Tom, T.D.; McNally, M.T.; Lowell, G.H.; Strand, M.
 J. Immunol. 149, 3612-3620, 1992
 A:Title: Induction of protective immunity in mice using a 62-kDa recombinant fragment
 A:Reference number: A46514; MUID:93056536; PMID:1431131
 A:Accession: S33068
 A:Molecule type: mRNA
 A:Residues: 1-527 <SOI>
 A:Cross-references: EMBL:X65591
 A:Note: the authors translated the codon CAA for residue 346 as Lys
 C:Superfamily: myosin heavy chain; myosin motor domain homology
 C:Keywords: ATP; surface antigen

Query Match 23.0%; Score 55.5; DB 2; Length 527;
 Best Local Similarity 30.8%; Pred. No. 25;
 Matches 12; Conservative 7; Mismatches 9; Indels 11; Gaps 2;

QY 1 ILKKWPMW-----PW---RRKHEAPEAPEIMILK 28
 DB 106 VLKNWPMWRLYTKVKKPMLNIAOEEEMKKADELAKLKE 144

Search completed: December 11, 2002, 15:40:25
 Job time: 21 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 11, 2002, 15:39:44 ; Search time 11 Seconds

(without alignments)
54.633 Million cell updates/sec

Title: US-09-444-281-35-27-35

Perfect score: 241

Sequence: 1 ILKKWPMWPMRRKHEAPEAPIMILKKWPMWPMRRK 37

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 103943 seqs, 16242309 residues

Total number of hits satisfying chosen parameters: 103943

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications-AA:*

1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	141.5	58.7	28	10	US-09-030-619-104
2	137.5	57.1	28	10	US-09-030-619-50
3	99	41.1	21	10	US-09-030-619-69
4	98	40.7	21	10	US-09-030-619-52
5	93.5	38.8	20	10	US-09-030-619-51
6	91	37.8	13	10	US-09-030-619-95
7	91	37.8	13	10	US-09-030-619-99
8	91	37.8	14	10	US-09-030-619-72
9	91	37.8	14	10	US-09-030-619-108
10	87.5	36.3	21	10	US-09-030-619-47
11	87	36.1	12	10	US-09-030-619-67
12	86	35.7	12	10	US-09-030-619-112
13	86	35.7	13	10	US-09-030-619-53
14	86	35.7	13	10	US-09-030-619-107
15	86	35.7	13	10	US-09-030-619-109
16	86	35.7	14	10	US-09-030-619-54
17	86	35.7	14	10	US-09-030-619-110
18	85	35.3	12	10	US-09-030-619-73
19	85	35.3	13	10	US-09-030-619-41

	20	85	35.3	13	10	US-09-030-619-103	Sequence 103, App
	21	83.5	34.6	15	10	US-09-030-619-39	Sequence 39, App1
	22	83	34.4	12	10	US-09-030-619-44	Sequence 44, App1
	23	83	34.4	13	10	US-09-030-619-105	Sequence 105, App
	24	83	34.4	13	10	US-09-030-619-106	Sequence 106, App
	25	83	34.4	20	10	US-09-030-619-24	Sequence 24, App1
	26	82.5	34.2	21	10	US-09-030-619-48	Sequence 48, App1
	27	82.5	34.0	13	10	US-09-030-619-58	Sequence 58, App1
	28	82	34.0	13	10	US-09-030-619-59	Sequence 59, App1
	29	82	34.0	13	10	US-09-030-619-94	Sequence 94, App1
	30	82	34.0	13	10	US-09-030-619-102	Sequence 102, App
	31	81	33.6	11	10	US-09-030-619-79	Sequence 79, App1
	32	81	33.6	11	10	US-09-030-619-114	Sequence 114, App
	33	78	32.4	11	10	US-09-030-619-78	Sequence 78, App1
	34	78	32.4	11	10	US-09-030-619-113	Sequence 113, App
	35	78	32.4	12	10	US-09-030-619-43	Sequence 43, App1
	36	77.5	32.2	12	10	US-09-030-619-40	Sequence 40, App1
	37	77	32.0	12	10	US-09-030-619-82	Sequence 82, App1
	38	76	31.5	12	10	US-09-030-619-82	Sequence 82, App1
	39	75	31.1	12	10	US-09-030-619-23	Sequence 23, App1
	40	75	31.1	12	10	US-09-030-619-30	Sequence 30, App1
	41	75	31.1	12	10	US-09-030-619-111	Sequence 111, App
	42	73.5	30.5	12	10	US-09-030-619-75	Sequence 75, App1
	43	73.5	30.5	12	10	US-09-030-619-76	Sequence 76, App1
	44	73	30.3	9	10	US-09-030-619-80	Sequence 80, App1
	45	73	30.3	10	10	US-09-030-619-81	Sequence 81, App1

ALIGNMENTS

RESULT 1
US-09-030-619-104
; Sequence 104, Application US/09030619B
; Patent No. US20020035061A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Timothy J.
; APPLICANT: Taylor, Robert
; APPLICANT: Ertler, Douglas
; APPLICANT: Fraser, Janet R.
; APPLICANT: West, Michael H.P.
; APPLICANT: McNicol, Patricia J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
; TITLE OF INVENTION: WITH ANTIBIOTICS
; FILE REFERENCE: 660081.406
; CURRENT APPLICATION NUMBER: US/09/030,619B
; CURRENT FILING DATE: 1998-02-25
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 104
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cationic Peptide Analogue
US-09-030-619-104

Query Match 58.7%; Score 141.5; DB 10; Length 28;
Best Local Similarity 58.8%; Pred. No. 4.8e-11;
Matches 20; Conservative 2; Mismatches 1; Indels 11; Gaps 1;

QY 4 KWPMPWPMRRKHEAPEAPIMILKKWPMWPMRRK 37
:||||||| :|||||||
Db 3 RWPMPWPMRRK-----ILMRWPMWPMRRK 25

RESULT 2
US-09-030-619-50
; Sequence 50, Application US/09030619B
; Patent No. US20020035061A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Timothy J.

```

: APPLICANT: Taylor, Robert
: APPLICANT: Erfile, Douglas
: APPLICANT: Fraser, Janet R.
: APPLICANT: West, Michael H.P.
: APPLICANT: McNICOL, Patricia J.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
: TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
: TITLE OF INVENTION: WITH ANTI-BIOTICS
: FILE REFERENCE: 660081.406
: CURRENT APPLICATION NUMBER: US/09/030,619B
: CURRENT FILING DATE: 1998-02-25
: NUMBER OF SEQ ID NOS: 232
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 50
: LENGTH: 28
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Indollicidin Analogue
US-09-030-619-50
```

```

Query Match          57.1%; Score 137.5; DB 10; Length 28;
Best Local Similarity 61.8%; Pred. No. 1.4e-10;
Matches 21; Conservative 2; Mismatches 0; Indels 11; Gaps 2;
```

```
Qy 4 ILKKPMPWPRRKHEAPEAPIMILKKMPWPRRK 37
Db 3 RWPMPWPRRK-----MIL-RMPMPWPRRK 25
```

```

RESULT 3
US-09-030-619-69
: Sequence 69, Application US/09030619B
: Patent No. US20020035061A1
: GENERAL INFORMATION:
: APPLICANT: Krieger, Timothy J.
: APPLICANT: Taylor, Robert
: APPLICANT: Erfile, Douglas
: APPLICANT: Fraser, Janet R.
: APPLICANT: West, Michael H.P.
: APPLICANT: McNICOL, Patricia J.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
: TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
: TITLE OF INVENTION: WITH ANTI-BIOTICS
: FILE REFERENCE: 660081.406
: CURRENT APPLICATION NUMBER: US/09/030,619B
: CURRENT FILING DATE: 1998-02-25
: NUMBER OF SEQ ID NOS: 232
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 69
: LENGTH: 21
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Indollicidin Analogue
US-09-030-619-69
```

```

Query Match          41.1%; Score 99; DB 10; Length 21;
Best Local Similarity 64.3%; Pred. No. 3.6e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 10; Gaps 1;
```

```
Qy 1 ILKKPMPWPRRKHEAPEAPIMILKK 28
Db 1 ILKKPMPWPRRK-----MILKK 18
```

```

RESULT 4
US-09-030-619-52
: Sequence 52, Application US/09030619B
: Patent No. US20020035061A1
: GENERAL INFORMATION:
: APPLICANT: Krieger, Timothy J.
: APPLICANT: Taylor, Robert
: APPLICANT: Erfile, Douglas
```

```

: APPLICANT: Erfile, Douglas
: APPLICANT: Fraser, Janet R.
: APPLICANT: West, Michael H.P.
: APPLICANT: McNICOL, Patricia J.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
: TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
: TITLE OF INVENTION: WITH ANTI-BIOTICS
: FILE REFERENCE: 660081.406
: CURRENT APPLICATION NUMBER: US/09/030,619B
: CURRENT FILING DATE: 1998-02-25
: NUMBER OF SEQ ID NOS: 232
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 52
: LENGTH: 21
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Indollicidin Analogue
US-09-030-619-52
```

```

Query Match          40.7%; Score 98; DB 10; Length 21;
Best Local Similarity 64.3%; Pred. No. 4.7e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 10; Gaps 1;
```

```
Qy 1 ILKKPMPWPRRKHEAPEAPIMILKK 28
Db 1 ILKKPMPWPRRK-----IMILKK 18
```

```

RESULT 5
US-09-030-619-51
: Sequence 51, Application US/09030619B
: Patent No. US20020035061A1
: GENERAL INFORMATION:
: APPLICANT: Krieger, Timothy J.
: APPLICANT: Taylor, Robert
: APPLICANT: Erfile, Douglas
: APPLICANT: Fraser, Janet R.
: APPLICANT: West, Michael H.P.
: APPLICANT: McNICOL, Patricia J.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
: TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
: TITLE OF INVENTION: WITH ANTI-BIOTICS
: FILE REFERENCE: 660081.406
: CURRENT APPLICATION NUMBER: US/09/030,619B
: CURRENT FILING DATE: 1998-02-25
: NUMBER OF SEQ ID NOS: 232
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 51
: LENGTH: 20
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Indollicidin Analogue
US-09-030-619-51
```

```

Query Match          38.8%; Score 93.5; DB 10; Length 20;
Best Local Similarity 60.7%; Pred. No. 1.5e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 11; Gaps 1;
```

```
Qy 1 ILKKPMPWPRRKHEAPEAPIMILKK 28
Db 1 ILKKPMPWPRRK-----MILKK 17
```

```

RESULT 6
US-09-030-619-95
: Sequence 95, Application US/09030619B
: Patent No. US20020035061A1
: GENERAL INFORMATION:
: APPLICANT: Krieger, Timothy J.
: APPLICANT: Taylor, Robert
: APPLICANT: Erfile, Douglas
```



```
; APPLICANT: Fraser, Janet R.
; APPLICANT: West, Michael H.P.
; APPLICANT: McNicol, Patricia J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
; TITLE OF INVENTION: WITH ANTIBIOTICS
; FILE REFERENCE: 660081.406
; CURRENT APPLICATION NUMBER: US/09/030,619B
; CURRENT FILING DATE: 1998-02-25
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 95
; LENGTH: 13
; TYPE: PRP
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cationic Peptide Analogue
US-09-030-619-95
```

```
Query Match          37.8%; Score 91; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 ILKKPMPMPRRK 13
        |||
Db      1 ILKKPMPMPRRK 13
```

```
RESULT 7
US-09-030-619-99
; Sequence 99, Application US/09030619B
; Patent No. US20020035061A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Timothy J.
; APPLICANT: Taylor, Robert
; APPLICANT: Erfile, Douglas
; APPLICANT: Fraser, Janet R.
; APPLICANT: West, Michael H.P.
; APPLICANT: McNicol, Patricia J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
; TITLE OF INVENTION: WITH ANTIBIOTICS
; FILE REFERENCE: 660081.406
; CURRENT APPLICATION NUMBER: US/09/030,619B
; CURRENT FILING DATE: 1998-02-25
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 99
; LENGTH: 13
; TYPE: PRP
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cationic Peptide Analogue
US-09-030-619-99
```

```
Query Match          37.8%; Score 91; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 ILKKPMPMPRRK 13
        |||
Db      1 ILKKPMPMPRRK 13
```

```
RESULT 8
US-09-030-619-72
; Sequence 72, Application US/09030619B
; Patent No. US20020035061A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Timothy J.
; APPLICANT: Taylor, Robert
; APPLICANT: Erfile, Douglas
; APPLICANT: Fraser, Janet R.
```

```
; APPLICANT: West, Michael H.P.
; APPLICANT: McNicol, Patricia J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
; TITLE OF INVENTION: WITH ANTIBIOTICS
; FILE REFERENCE: 660081.406
; CURRENT APPLICATION NUMBER: US/09/030,619B
; CURRENT FILING DATE: 1998-02-25
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 72
; LENGTH: 14
; TYPE: PRP
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Indolicidin Analogue
US-09-030-619-72
```

```
Query Match          37.8%; Score 91; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 ILKKPMPMPRRK 13
        |||
Db      1 ILKKPMPMPRRK 13
```

```
RESULT 9
US-09-030-619-108
; Sequence 108, Application US/09030619B
; Patent No. US20020035061A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Timothy J.
; APPLICANT: Taylor, Robert
; APPLICANT: Erfile, Douglas
; APPLICANT: Fraser, Janet R.
; APPLICANT: West, Michael H.P.
; APPLICANT: McNicol, Patricia J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
; TITLE OF INVENTION: WITH ANTIBIOTICS
; FILE REFERENCE: 660081.406
; CURRENT APPLICATION NUMBER: US/09/030,619B
; CURRENT FILING DATE: 1998-02-25
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 108
; LENGTH: 14
; TYPE: PRP
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cationic Peptide Analogue
US-09-030-619-108
```

```
Query Match          37.8%; Score 91; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 ILKKPMPMPRRK 13
        |||
Db      1 ILKKPMPMPRRK 13
```

```
RESULT 10
US-09-030-619-47
; Sequence 47, Application US/09030619B
; Patent No. US20020035061A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Timothy J.
; APPLICANT: Taylor, Robert
; APPLICANT: Erfile, Douglas
; APPLICANT: Fraser, Janet R.
```

```

; APPLICANT: McNicol, Patricia J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
; TITLE OF INVENTION: WITH ANTIBIOTICS
; FILE REFERENCE: 660081.406
; CURRENT APPLICATION NUMBER: US/09/030.619B
; CURRENT FILING DATE: 1998-02-25
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 47
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Indoliciidin Analogue
US-09-030-619-47

Query Match          36.3%; Score 87.5; DB 10; Length 21;
Best Local Similarity 60.0%; Pred. No. 8.1e-05;
Matches 15; Conservative 1; Mismatches 0; Indels 9; Gaps 1;

QY      4  KWPWPWRRKHEAPPEPIMILKK 28
        :|||||
Db      3  RWPWPWRRK-----IMILKK 18

RESULT 11
US-09-030-619-67
; Sequence 67, Application US/09030619B
; Patent No. US20020035061A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Timothy J.
; APPLICANT: Taylor, Robert
; APPLICANT: Erile, Douglas
; APPLICANT: Fraser, Janet R.
; APPLICANT: West, Michael H.P.
; APPLICANT: McNicol, Patricia J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
; TITLE OF INVENTION: WITH ANTIBIOTICS
; FILE REFERENCE: 660081.406
; CURRENT APPLICATION NUMBER: US/09/030.619B
; CURRENT FILING DATE: 1998-02-25
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 67
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Indoliciidin Analogue
US-09-030-619-67

Query Match          36.1%; Score 87; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.1e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2  LKKWPWPWRRK 13
        :|||||
Db      1  LKKWPWPWRRK 12

RESULT 12
US-09-030-619-112
; Sequence 112, Application US/09030619B
; Patent No. US20020035061A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Timothy J.
; APPLICANT: Taylor, Robert
; APPLICANT: Erile, Douglas
; APPLICANT: Fraser, Janet R.
; APPLICANT: West, Michael H.P.
; APPLICANT: McNicol, Patricia J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
```

```

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
; TITLE OF INVENTION: WITH ANTIBIOTICS
; FILE REFERENCE: 660081.406
; CURRENT APPLICATION NUMBER: US/09/030.619B
; CURRENT FILING DATE: 1998-02-25
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 112
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cationic Peptide Analogue
US-09-030-619-112

Query Match          35.7%; Score 86; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.7e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  ILKKWPWPWRR 12
        :|||||
Db      1  ILKKWPWPWRR 12

RESULT 13
US-09-030-619-53
; Sequence 53, Application US/09030619B
; Patent No. US20020035061A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Timothy J.
; APPLICANT: Taylor, Robert
; APPLICANT: Erile, Douglas
; APPLICANT: Fraser, Janet R.
; APPLICANT: West, Michael H.P.
; APPLICANT: McNicol, Patricia J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
; TITLE OF INVENTION: WITH ANTIBIOTICS
; FILE REFERENCE: 660081.406
; CURRENT APPLICATION NUMBER: US/09/030.619B
; CURRENT FILING DATE: 1998-02-25
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 53
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Indoliciidin Analogue
US-09-030-619-53

Query Match          35.7%; Score 86; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 7.3e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  ILKKWPWPWRR 12
        :|||||
Db      1  ILKKWPWPWRR 12

RESULT 14
US-09-030-619-107
; Sequence 107, Application US/09030619B
; Patent No. US20020035061A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Timothy J.
; APPLICANT: Taylor, Robert
; APPLICANT: Erile, Douglas
; APPLICANT: Fraser, Janet R.
; APPLICANT: West, Michael H.P.
; APPLICANT: McNicol, Patricia J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
```

;; TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
;; TITLE OF INVENTION: WITH ANTIBIOTICS
;; FILE REFERENCE: 660081.406
;; CURRENT APPLICATION NUMBER: US/09/030,619B
;; CURRENT FILING DATE: 1998-02-25
;; NUMBER OF SEQ ID NOS: 232
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 107
;; LENGTH: 13
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Cationic Peptide Analogue
US-09-030-619-107

Query Match 35.7%; Score 86; DB 10; Length 13;
Best Local Similarity 41.9%; Pred. No. 7.3e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 18; Gaps 1;

OY 7 WMPWRKHAEPEAPIMILKKMPMPWRK 37
|| |||||
Db 1 WW-----KKMPMPWRK 13

RESULT 15
US-09-030-619-109
; Sequence 109, Application US/09030619B
; Patent No. US20020035061A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Timothy J.
; APPLICANT: Taylor, Robert
; APPLICANT: Erle, Douglas
; APPLICANT: Fraser, Janet R.
; APPLICANT: West, Michael H.P.
; APPLICANT: McNicol, Patricia J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
; TITLE OF INVENTION: WITH ANTIBIOTICS
; FILE REFERENCE: 660081.406
; CURRENT APPLICATION NUMBER: US/09/030,619B
; CURRENT FILING DATE: 1998-02-25
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 109
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cationic Peptide Analogue
US-09-030-619-109

Query Match 35.7%; Score 86; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 7.3e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ILKKMPMPWR 12
|||||
Db 1 ILKKMPMPWR 12

Search completed: December 11, 2002, 15:43:29
Job time : 11 secs

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OM protein - protein search, using sw model

Run on: December 11, 2002, 15:37:49 : Search time 15 seconds

(without alignments)
72.577 Million cell updates/sec

Title: US-09-444-281-35-27-35

Sequence: 1 ILKKWPMWPMRRKHEAPEEPIMLKKWPMWPMRRK 37

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Issued Patents AA:*

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2: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
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5: /cgn2_6/prodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/1/1aa/backfilest1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	133.5	55.4	63	4	US-09-099-631A-12
2	99.5	41.3	16	4	US-08-702-054B-38
3	99	41.1	21	4	US-08-915-314-54
4	98	40.7	21	4	US-08-915-314-56
5	93.5	38.8	20	4	US-08-915-314-55
6	91	37.8	13	4	US-08-915-314-30
7	91	37.8	13	4	US-08-915-314-62
8	91	37.8	13	4	US-08-915-314-63
9	91	37.8	13	4	US-08-915-314-64
10	91	37.8	13	4	US-08-915-314-65
11	91	37.8	14	4	US-09-042-071-36
12	89	36.9	15	4	US-08-915-314-57
13	87.5	36.3	21	4	US-08-702-054B-40
14	87	36.1	12	4	US-08-915-314-46
15	86	35.7	12	4	US-08-915-314-52
16	86	35.7	12	4	US-08-915-314-74
17	86	35.7	12	4	US-08-702-054B-5
18	86	35.7	13	4	US-08-915-314-51
19	86	35.7	13	4	US-08-915-314-58
20	86	35.7	14	4	US-08-702-054B-34
21	85.5	35.5	16	4	US-08-915-314-59
22	85	35.3	12	4	US-08-702-054B-11
23	85	35.3	13	4	US-08-915-314-69
24	85	35.3	13	4	US-08-915-314-38
25	85	35.3	13	4	US-08-915-314-45
26	85	35.3	13	4	US-08-702-054B-17
27	85	35.3	13	4	US-08-702-054B-32

28	83.5	34.6	15	4	US-08-702-054B-39	Sequence 39, Appl
29	83	34.4	12	4	US-08-915-314-24	Sequence 24, Appl
30	83	34.4	13	4	US-08-915-314-49	Sequence 49, Appl
31	83	34.4	13	4	US-08-915-314-50	Sequence 50, Appl
32	83	34.4	13	4	US-08-702-054B-30	Sequence 30, Appl
33	83	34.4	13	4	US-08-702-054B-31	Sequence 31, Appl
34	83	34.4	13	4	US-08-702-054B-35	Sequence 35, Appl
35	83	34.4	20	4	US-08-915-314-47	Sequence 47, Appl
36	82.5	34.2	21	4	US-08-915-314-48	Sequence 48, Appl
37	82	34.0	13	4	US-08-915-314-25	Sequence 25, Appl
38	82	34.0	13	4	US-08-915-314-66	Sequence 66, Appl
39	82	34.0	13	4	US-08-915-314-67	Sequence 67, Appl
40	82	34.0	13	4	US-08-702-054B-33	Sequence 33, Appl
41	81	33.6	11	4	US-08-915-314-75	Sequence 75, Appl
42	80	33.2	14	4	US-08-702-054B-18	Sequence 18, Appl
43	80	33.2	15	4	US-08-702-054B-41	Sequence 41, Appl
44	80	33.2	16	4	US-08-702-054B-2	Sequence 2, Appl
45	79	32.8	17	4	US-08-702-054B-42	Sequence 42, Appl

ALIGNMENTS

```
RESULT 1
US-09-099-631A-12
; Sequence 12, Application US/09099631A
; Patent No. 6444645
; GENERAL INFORMATION:
; APPLICANT: Selsled, Michael E.
; TITLE OF INVENTION: Crosslink-Stabilized Indollicidin Analogs
; FILE REFERENCE: P-UC 3050
; CURRENT APPLICATION NUMBER: US/09/099, 631A
; CURRENT FILING DATE: 1998-06-18
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-099-631A-12

Query Match      55.4%; Score 133.5; DB 4; Length 63;
Best Local Similarity 64.7%; Pred. No. 2.9e-10;
Matches 22; Conservative 0; Mismatches 5; Indels 7; Gaps 2;

QY      4  KWPMPWPMRRKHEAPEEPIMLK-KWPMPWPMRR 36
Db      11 KWPMPWPMRRM-----ARIAMILPWPMPWPMRR 38

RESULT 2
US-08-702-054B-38
; Sequence 38, Application US/08702054B
; Patent No. 6191254
; GENERAL INFORMATION:
; APPLICANT: Falls, Timothy J.
; APPLICANT: Hancock, Robert E. W.
; TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDES
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
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COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/702,054B
FILING DATE: 23-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/002,687
FILING DATE: 23-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07420/013001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-702-054B-38

Query Match 41.3%; Score 99.5; DB 4; Length 16;
Best Local Similarity 43.2%; Pred. No. 1.2e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 21; Gaps 1;

QY 1 ILKKPWPWRRKHEAPEAPIMILKKPWPWRRK 37
DB 1 ILKKPWPWRRKHEAPEAPIMILKKPWPWRRK 16

RESULT 3
US-08-915-314-54
Sequence 54, Application US/08915314
Patent No. 6180604
GENERAL INFORMATION:
APPLICANT: Fraser, Janet R.
APPLICANT: West, Michael H.P.
APPLICANT: Krieger, Timothy J.
APPLICANT: Taylor, Robert
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS USING ANALOGUES OF INOLICIDIN
NUMBER OF SEQUENCES: 90
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,314
FILING DATE: 20-AUG-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: No. 6180604tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 660081.405
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid

STRANDEDNESS:
TOPOLOGY: linear
US-08-915-314-54

Query Match 41.1%; Score 99; DB 4; Length 21;
Best Local Similarity 64.3%; Pred. No. 1.9e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

QY 1 ILKKPWPWRRKHEAPEAPIMILKK 28
DB 1 ILKKPWPWRRKHEAPEAPIMILKK 18

RESULT 4
US-08-915-314-56
Sequence 56, Application US/08915314
Patent No. 6180604
GENERAL INFORMATION:
APPLICANT: Fraser, Janet R.
APPLICANT: West, Michael H.P.
APPLICANT: Krieger, Timothy J.
APPLICANT: Taylor, Robert
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS USING ANALOGUES OF INOLICIDIN
NUMBER OF SEQUENCES: 90
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,314
FILING DATE: 20-AUG-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: No. 6180604tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 660081.405
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-915-314-56

Query Match 40.7%; Score 98; DB 4; Length 21;
Best Local Similarity 64.3%; Pred. No. 2.3e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

QY 1 ILKKPWPWRRKHEAPEAPIMILKK 28
DB 1 ILKKPWPWRRKHEAPEAPIMILKK 18

RESULT 5
US-08-915-314-55
Sequence 55, Application US/08915314
Patent No. 6180604
GENERAL INFORMATION:
APPLICANT: Fraser, Janet R.
APPLICANT: West, Michael H.P.

APPLICANT: Krieger, Timothy J.
APPLICANT: Taylor, Robert
APPLICANT: Erfile, Douglas
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
NUMBER OF SEQUENCES: 90
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,314
FILING DATE: 20-AUG-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: No. 6180604tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 660081.405
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
US-08-915-314-55

Query Match 38.8%; Score 93.5; DB 4; Length 20;
Best Local Similarity 60.7%; Pred. No. 8 8e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 11; Gaps 1;

OY 1 ILKKPMPWRRKHEAPEAEPIMILKK 28
Db 1 ILKKPMPWRR-----MILKK 17

RESULT 6
US-08-915-314-30
Sequence 30, Application US/08915314
Patent No. 6180604
GENERAL INFORMATION:
APPLICANT: Fraser, Janet R.
APPLICANT: West, Michael H.P.
APPLICANT: Krieger, Timothy J.
APPLICANT: Taylor, Robert
APPLICANT: Erfile, Douglas
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
NUMBER OF SEQUENCES: 90
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,314

FILING DATE: 20-AUG-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: No. 6180604tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 660081.405
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
US-08-915-314-30

Query Match 37.8%; Score 91; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ILKKPMPWRRK 13
Db 1 ILKKPMPWRRK 13

RESULT 7
US-08-915-314-62
Sequence 62, Application US/08915314
Patent No. 6180604
GENERAL INFORMATION:
APPLICANT: Fraser, Janet R.
APPLICANT: West, Michael H.P.
APPLICANT: Krieger, Timothy J.
APPLICANT: Taylor, Robert
APPLICANT: Erfile, Douglas
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
NUMBER OF SEQUENCES: 90
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,314
FILING DATE: 20-AUG-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: No. 6180604tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 660081.405
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
FEATURE: Modified-site
NAME/KEY: 1
LOCATION: 1
OTHER INFORMATION: /note= "D-Form of Isoleucine"
US-08-915-314-62

Query Match 37.8%; Score 91; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILKKPMPWRRK 13
DB 1 ILKKPMPWRRK 13

RESULT 8
US-08-915-314-63
; Sequence 63, Application US/08915314
; Patent No. 6180604
; GENERAL INFORMATION:
; APPLICANT: Fraser, Janet R.
; APPLICANT: West, Michael H.P.
; APPLICANT: Krieger, Timothy J.
; APPLICANT: Taylor, Robert
; APPLICANT: Effie, Douglas
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS USING ANALOGUES OF INDOLICIDIN
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/915,314
; FILING DATE: 20-AUG-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6180604tenburg Ph.D., Carol
; REGISTRATION NUMBER: 39,317
; REFERENCE/DOCKET NUMBER: 660081.405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 13
; OTHER INFORMATION: /note="D-Form of Lysine"
US-08-915-314-63

Query Match 37.8%; Score 91; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILKKPMPWRRK 13
DB 1 ILKKPMPWRRK 13

RESULT 9
US-08-915-314-64
; Sequence 64, Application US/08915314
; Patent No. 6180604
; GENERAL INFORMATION:
; APPLICANT: Fraser, Janet R.

APPLICANT: West, Michael H.P.
APPLICANT: Krieger, Timothy J.
APPLICANT: Taylor, Robert
APPLICANT: Effie, Douglas
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS USING ANALOGUES OF INDOLICIDIN
NUMBER OF SEQUENCES: 90
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,314
FILING DATE: 20-AUG-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: No. 6180604tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 660081.405
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /note="D-Form of Isoleucine"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 13
OTHER INFORMATION: /note="D-Form of Lysine"
US-08-915-314-64

Query Match 37.8%; Score 91; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILKKPMPWRRK 13
DB 1 ILKKPMPWRRK 13

RESULT 10
US-09-042-071-36
; Sequence 36, Application US/09042071
; Patent No. 6294372
; GENERAL INFORMATION:
; APPLICANT: Burian, Jan
; APPLICANT: Kay, William W.
; TITLE OF INVENTION: REPLICATION GENES AND GENE PRODUCTS FROM
; TITLE OF INVENTION: SMALL CRYPTIC PLASMIDS AND METHODS FOR CONSTRUCTING
; TITLE OF INVENTION: CONTROLLED-REPLICATION PLASMID VECTORS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104


```

;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,071
; FILING DATE: 13-MAR-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 660081.407
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-09-042-071-36
;
Query Match
; 37.8%; Score 91; DB 4; Length 13;
; Best Local Similarity 100.0%; Pred. No. 1.1e-05;
; Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 1 ILKKPWPWPWRRK 13
;
Db 1 ILKKPWPWPWRRK 13
;
RESULT 11
US-08-915-314-57
; Sequence 57, Application US/08915314
; Patent No. 6180604
; GENERAL INFORMATION:
; APPLICANT: Fraser, Janet R.
; APPLICANT: West, Michael H.P.
; APPLICANT: Krieger, Timothy J.
; APPLICANT: Taylor, Robert
; APPLICANT: Erfile, Douglas
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS USING ANALOGUES OF INDOLICIDIN
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/915,314
; FILING DATE: 20-AUG-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6180604tenburg, Ph.D., Carol
; REGISTRATION NUMBER: 39,317
; REFERENCE/DOCKET NUMBER: 660081.405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-915-314-57
;
Query Match
; 37.8%; Score 91; DB 4; Length 13;
; Best Local Similarity 100.0%; Pred. No. 1.1e-05;
; Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 1 ILKKPWPWPWRRK 13
;
Db 1 ILKKPWPWPWRRK 13
;
RESULT 12
US-08-702-054B-40
; Sequence 40, Application US/08702054B
; Patent No. 6191254
; GENERAL INFORMATION:
; APPLICANT: Falls, Timothy J.
; APPLICANT: Hancock, Robert E. W.
; APPLICANT: Gough, Monisha
; TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDES
; TITLE OF INVENTION: AND METHODS OF SCREENING FOR THE SAME
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/702,054B
; FILING DATE: 23-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/002,687
; FILING DATE: 23-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Halle, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07420/013001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-08-702-054B-40
;
Query Match
; 36.9%; Score 89; DB 4; Length 15;
; Best Local Similarity 43.8%; Pred. No. 2.4e-05;
; Matches 14; Conservative 0; Mismatches 0; Indels 18; Gaps 1;
;
QY 1 ILKKPWPWPWRRKHAPEPEPIILKKPWPW 32
;
Db 1 ILKKPWPWPWRRK-----HW 14
;
RESULT 13
US-08-915-314-46
; Sequence 46, Application US/08915314
; Patent No. 6180604
; GENERAL INFORMATION:
; APPLICANT: Fraser, Janet R.
; APPLICANT: West, Michael H.P.
```

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;
; STRANDEDNESS:
; TOPOLOGY: linear
;
US-08-915-314-57
;
Query Match
; 37.8%; Score 91; DB 4; Length 14;
; Best Local Similarity 100.0%; Pred. No. 1.2e-05;
; Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 1 ILKKPWPWPWRRK 13
;
Db 1 ILKKPWPWPWRRK 13
;
RESULT 12
US-08-702-054B-40
; Sequence 40, Application US/08702054B
; Patent No. 6191254
; GENERAL INFORMATION:
; APPLICANT: Falls, Timothy J.
; APPLICANT: Hancock, Robert E. W.
; APPLICANT: Gough, Monisha
; TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDES
; TITLE OF INVENTION: AND METHODS OF SCREENING FOR THE SAME
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/702,054B
; FILING DATE: 23-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/002,687
; FILING DATE: 23-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Halle, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07420/013001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-08-702-054B-40
;
Query Match
; 36.9%; Score 89; DB 4; Length 15;
; Best Local Similarity 43.8%; Pred. No. 2.4e-05;
; Matches 14; Conservative 0; Mismatches 0; Indels 18; Gaps 1;
;
QY 1 ILKKPWPWPWRRKHAPEPEPIILKKPWPW 32
;
Db 1 ILKKPWPWPWRRK-----HW 14
;
RESULT 13
US-08-915-314-46
; Sequence 46, Application US/08915314
; Patent No. 6180604
; GENERAL INFORMATION:
; APPLICANT: Fraser, Janet R.
; APPLICANT: West, Michael H.P.
```

APPLICANT: Krieger, Timothy J.
APPLICANT: Taylor, Robert
APPLICANT: Erfile, Douglas
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS USING ANALOGUES OF INDOLICIDIN
NUMBER OF SEQUENCES: 90
CORRESPONDENCE ADDRESS:
ADDRESS: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,314
FILING DATE: 20-AUG-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: No. 6180604tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 660081.405
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 622-6031
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-915-314-46
Query Match 36.3%; Score 87.5; DB 4; Length 21;
Best Local Similarity 60.0%; Pred. No. 5.2e-05;
Matches 15; Conservative 1; Mismatches 0; Indels 9; Gaps 1;
OY 4 KWPMPWRRRHEAPEAPIMILKK 28
:|||||
Db 3 RWPMPWRRK-----IMILKK 18
RESULT 14
US-08-915-314-52
Sequence 52, Application US/08915314
Patent No. 6180604
GENERAL INFORMATION:
APPLICANT: Fraser, Janet R.
APPLICANT: West, Michael H.P.
APPLICANT: Krieger, Timothy J.
APPLICANT: Taylor, Robert
APPLICANT: Erfile, Douglas
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS USING ANALOGUES OF INDOLICIDIN
NUMBER OF SEQUENCES: 90
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COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,314

FILING DATE: 20-AUG-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: No. 6180604tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 660081.405
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 622-6031
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-915-314-52
Query Match 36.1%; Score 87; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.3e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2 LKKPMPWRRK 13
:|||||
Db 1 LKKPMPWRRK 12
RESULT 15
US-08-915-314-74
Sequence 74, Application US/08915314
Patent No. 6180604
GENERAL INFORMATION:
APPLICANT: Fraser, Janet R.
APPLICANT: West, Michael H.P.
APPLICANT: Krieger, Timothy J.
APPLICANT: Taylor, Robert
APPLICANT: Erfile, Douglas
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS USING ANALOGUES OF INDOLICIDIN
NUMBER OF SEQUENCES: 90
CORRESPONDENCE ADDRESS:
ADDRESS: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,314
FILING DATE: 20-AUG-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: No. 6180604tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 660081.405
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 622-6031
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-915-314-74
Query Match 35.7%; Score 86; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.5e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILKKPWPWPWR 12
| | | | | | | | | |
Db 1 ILKKPWPWPWR 12

Search completed: December 11, 2002, 15:39:59
Job time : 16 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 11, 2002, 15:34:29 ; Search time 35 seconds
(without alignments)
140.865 Million cell updates/sec

Title: US-09-444-281-35-27-35
Perfect score: 241
Sequence: 1 ILKKWPMWPMRRKHEAPEPIMILKKWPMWPMRRK 37

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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- 2: /SID2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
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- 20: /SID2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
- 21: /SID2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
- 22: /SID2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
- 23: /SID2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	141.5	58.7	28	21	AAV91800
2	137.5	57.1	27	19	AAW66363
3	133.5	55.4	63	21	AAV44668
4	133.5	55.4	63	21	AAV57142
5	99.5	41.3	16	18	AAW12899
6	99.5	41.1	21	19	AAV24582
7	99	41.1	21	19	AAV91806
8	98	40.7	21	21	AAV24571
9	98	40.7	21	21	AAV91808
10	93.5	38.8	20	19	AAV24570

11	93.5	38.8	20	21	AAV91807
12	91	37.8	13	18	AAW12873
13	91	37.8	13	19	AAV24609
14	91	37.8	13	19	AAW66378
15	91	37.8	13	19	AAW71690
16	91	37.8	13	21	AAV94495
17	91	37.8	13	21	AAV92795
18	91	37.8	13	21	AAV91773
19	91	37.8	13	21	AAV91774
20	91	37.8	13	21	AAV91818
21	91	37.8	13	21	AAV91819
22	91	37.8	13	21	AAV91820
23	91	37.8	13	23	ABB81254
24	91	37.8	14	19	AAV24583
25	91	37.8	14	21	AAV91811
26	89	36.9	15	18	AAW13802
27	87.5	36.3	21	19	AAV24552
28	87.5	36.3	21	19	AAW66376
29	87.5	36.3	21	21	AAV91796
30	87	36.1	12	19	AAV24580
31	87	36.1	12	21	AAV91804
32	86	35.7	12	18	AAW12877
33	86	35.7	12	19	AAV24615
34	86	35.7	12	21	AAV91833
35	86	35.7	13	18	AAW12896
36	86	35.7	13	19	AAV24613
37	86	35.7	13	19	AAV24572
38	86	35.7	13	21	AAV91803
39	86	35.7	13	21	AAV91812
40	86	35.7	14	19	AAV24573
41	86	35.7	14	21	AAV91813
42	85.5	35.5	16	18	AAW12882
43	85	35.3	12	19	AAV24586
44	85	35.3	12	21	AAV91828
45	85	35.3	13	18	AAW27179

ALIGNMENTS

RESULT 1	
ID	AAV91800 standard; Peptide; 28 AA.
XX	
AC	AAV91800;
XX	
DT	06-JUN-2000 (first entry)
XX	
DE	Amino acid sequence of cationic peptide MBI 11B20CN.
XX	
KW	Cationic peptide; tumour; pharmaceutical composition; Cancer; treatment;
KW	Leukemia; polyoxalkylene-modified; APO; lymphoma; multiple myeloma;
KW	breast; lung; ovary; cervix; uterus; skin; prostate; liver; colon;
KW	multidrug resistance.
XX	
OS	Synthetic.
XX	
PN	WO965506-A2.
XX	
PD	23-DEC-1999.
XX	
PF	14-JUN-1999; 99WC-CA00552.
XX	
PR	12-JUN-1998; 98US-0096541.
XX	
PA	(MICR-) MICROLOGIX BIOTECH INC.
XX	
PI	Friedland HD, Krieger TJ, Taylor R, Erfile D, Fraser JR, West MHP;
XX	WPI; 2000-223549/19.
DR	
XX	
PT	Novel pharmaceutical composition containing optionally activated polyoxalkylene-modified cationic peptides, useful for treating tumours

DR N-PSDB; AA249764.
 XX Crosslinked indolicidin analogs with antimicrobial activity against
 PT bacteria, yeast, fungi, protozoa and viruses
 XX
 PS Example 1C; Fig 1; 53pp; English.
 XX
 CC The patent discloses crosslinked analogs of indolicidin (Indol 1-13)
 CC which is a naturally occurring peptide isolated from bovine neutrophils
 CC and has antimicrobial activity. The crosslinked indolicidin
 CC (X-indolicidin) analogs are stable and have antimicrobial activity
 CC against gram positive and negative bacteria (e.g. *Staphylococcus aureus*,
 CC *Escherichia coli* and *Salmonella typhimurium*), yeasts and fungi (e.g.
 CC *Candida albicans*, *Cryptococcus neoformans*), protozoa (e.g. *Giardia*
 CC species and *Acanthamoeba* species), and viruses (e.g. HIV-1).
 CC They can be used for reducing or inhibiting the growth or survival of
 CC microorganisms in an environment e.g. a food or food product, a
 CC solution, an inanimate object comprising a surface, or a mammal.
 CC The present sequence is a protein comprising three
 CC copies of Indol 1-13 each separated by a hexapeptide spacer sequence.
 CC A recombinant construct encoding this sequence was used for the
 CC expression of Indol-homoserine (Hse) analog. The ability of
 CC Indol-Hse analog to maintain antimicrobial activity provides a means to
 CC produce X-indolicidin analog precursors in sufficient quantities.
 CC
 SQ Sequence 63 AA;
 Query Match 55.4%; Score 133.5; DB 21; Length 63;
 Best Local Similarity 64.7%; Pred. No. 9e-10;
 Matches 22; Conservative 0; Mismatches 5; Indels 7; Gaps 2;
 OY 4 KWPMPWRRKHEAPEEPIMLK-KWPMPWRR 36
 ||||||| | ||| |||||||
 Db 11 KWPMPWRRM-----ARIAMILPWKWPMPWRR 38
 RESULT 4
 AA57142
 ID AA57142 standard; Protein; 63 AA.
 XX
 AC AA57142;
 XX
 DT 28-FEB-2000 (first entry)
 XX
 DE Indolicidin fusion peptide amino acid sequence.
 XX
 KW Indolicidin analogue; antimicrobial activity; helminth; bacteria; virus;
 KM treatment; inhibit growth; micro-organism; contact lens solution;
 XX transgenic plant; surgical instrument; yeast; fungi; protozoa.
 OS Synthetic.
 XX
 PN WO958141-A1.
 XX
 PD 18-NOV-1999.
 XX
 PF 05-MAY-1999; 99WO-US09942.
 XX
 PR 12-MAY-1998; 98US-0076227.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Selected ME:
 XX
 DR WPI; 2000-053028/04.
 DR N-PSDB; AA245123.
 XX
 PT New indolicidin analogues, active against bacteria, yeast, fungi,
 PT protozoa and virus, used for, e.g. treating infections -
 XX
 PS Disclosure; Fig 6; 62pp; English.
 XX
 CC This is the amino acid sequence of an example of a fusion protein which

CC consists of an indolicidin analogue linked to another peptide.
 CC Peptides AA57109-Y57138 and AA57143-Y57144 are new indolicidin
 CC analogues, which have a homoserine residue and/or a truncated amino
 CC terminal region. The analogues have the following amino acid sequence:
 CC Xaa1-Xaa2-Xaa3-Xaa4-Xaa5-Xaa6-Pro-Xaa6-Pro-Xaa6-Xaa7-Xaa8
 CC where:
 CC Xaa1 = Ile, Leu, Val, Ala, Gly or absent;
 CC Xaa2 = Ile, Leu, Val, Ala, Gly or absent;
 CC Xaa3 = Pro or absent;
 CC Xaa4 = Trp, Phe or absent;
 CC Xaa5 = Arg, Lys or absent;
 CC Xaa6 = Trp or Phe;
 CC Xaa7 = Arg, Lys or absent;
 CC Xaa8 = homoserine (Hse), Met, Met-Xaa9-Met or absent, and
 CC Xaa9 = at least one amino acid;
 CC provided that if Xaa1 is present, Xaa8 = Hse, Met or Met-Xaa9-Met;
 CC and further provided that: if Xaa2 is absent, Xaa1 is absent; if Xaa3 is
 CC absent, Xaa1 and Xaa2 are absent; if Xaa4 is absent, Xaa1, Xaa2 and Xaa3
 CC are absent; and if Xaa5 is absent, Xaa1, Xaa2, Xaa3 and Xaa4 are absent.
 CC The indolicidin analogues can be used to create a fusion polypeptide
 CC consisting of the analogue linked to a peptide. The indolicidin
 CC analogues have antimicrobial activity against gram positive bacteria,
 CC gram negative bacteria, yeast, fungus, protozoa and viruses (e.g. HIV-1).
 CC They are also active against helminths. The analogues can be used for
 CC reducing or inhibiting growth or survival of a microorganism. They can be
 CC used for treating infections. They can also be included in a liquid such
 CC as water or an aqueous solution, e.g. contact lens solution. The
 CC analogues have potential uses in food products, and in objects such as
 CC the surface of an instrument used to prepare food or to perform surgery.
 CC Transgenic plants or animals useful in the food industry can be produced
 CC by introducing a nucleic acid molecule encoding an indolicidin analogue
 CC into the germ-line cells of such organisms.
 CC
 SQ Sequence 63 AA;
 Query Match 55.4%; Score 133.5; DB 21; Length 63;
 Best Local Similarity 64.7%; Pred. No. 9e-10;
 Matches 22; Conservative 0; Mismatches 5; Indels 7; Gaps 2;
 OY 4 KWPMPWRRKHEAPEEPIMLK-KWPMPWRR 36
 ||||||| | ||| |||||||
 Db 11 KWPMPWRRM-----ARIAMILPWKWPMPWRR 38
 RESULT 5
 AAW12899
 ID AAW12899 standard; peptide; 16 AA.
 XX
 AC AAW12899;
 XX
 DT 10-DEC-1997 (first entry)
 XX
 DE Antimicrobial cationic peptide CP-26.
 XX
 KW Bacterial; viral; antitumour; food; preservative; inhibitor; growth;
 KM bacterium; yeast; endotoxaemia; sepsis; antibiotic; fungal;
 XX antiviral; *Candida albicans*; sterility; *Salmonella*; Yersinia;
 XX *Shigella*.
 OS Synthetic.
 XX
 PN WO9708199-A2.
 XX
 PD 06-MAR-1997.
 XX
 PF 23-AUG-1996; 96WO-IB00996.
 XX
 PR 23-AUG-1995; 95US-0002687.
 XX
 PA (UYBR-) UNIV BRITISH COLUMBIA.
 XX
 PI Falia TJ, Gough M, Hancock RW,
 XX

DR WPI: 1997-179179/16.

XX Cationic peptide(s) having anti-microbial activity - used for the
 PT inhibition of bacterial and viral growth, as an antitumour agent,
 PT and as a food preservative
 XX

PS Claim 3; Page 66; 89pp; English.

XX The present sequence represents a specifically claimed novel isolated
 CC cationic peptide which has antimicrobial activity. The amino acid
 CC sequence of antimicrobial cationic peptides (including the present
 CC sequence) is selected from: X1X1ProX2X3X2Pro(X2X2Pro)X2X3(X5)O;
 CC X1X1ProX2X3X4(X5)ProX2X3X3; X1X1X3(ProTrp)uX3X2X5X2X5(X5)O;
 CC X1X1X3X3X2Pro(X2X2Pro)X2(X5)m: where m = 1-5; n = 1-2; o = 2-5; r
 CC = 0-8; u = 0-1; X1 = Ile, Leu, Val, Phe, Tyr, Trp or Met; X2 = Trp or
 CC Phe; X3 = Arg or Lys; X4 = Trp or Lys; and X5 = Phe, Trp, Arg, Lys or
 CC Pro. The peptides are preferably amidated or carboxymethylated. The
 CC peptides may be used in methods for inhibiting the growth of a bacterium
 CC or yeast, or for inhibiting an endotoxaemia or sepsis associated
 CC disorder in a subject. The peptides have a broad activity against
 CC antibiotic resistant bacteria, combined with activity against the
 CC medically important fungus *Candida albicans*. In addition, the peptides
 CC are useful as antitumour agents and/or antiviral agents. The peptides
 CC may be used as sterilants or preservatives of materials susceptible to
 CC microbial or viral contamination, e.g. in processed foods to inhibit
 CC *Salmonella*, *Yersinia* and *Shigella*. The peptides are compact and tend to
 CC have a unique polypyrrolone type II extended helix structure that permits
 CC them to span the membrane with relatively few amino acids. The peptides
 CC possess the ability to work synergistically with antibiotics, and in
 CC addition, some of them possess anti-endotoxin activity.
 CC

XX Sequence 16 AA:
 -50

Query Match 41.3%; Score 99.5; DB 18; Length 16;
 Best Local Similarity 43.2%; Pred. No. 3.7e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 21; Gaps 1;

OY 1 ILKKPMPWMPRRKHAEPEAPIMILKKPMPWMPRRK 37
 |||||
 DB 1 ILKKPMPWMPRRKHAEPEAPIMILKKPMPWMPRRK 16

RESULT 6
 AAY24582
 ID AAY24582 standard; peptide; 21 AA.
 AC AAY24582;
 XX
 DT 18-AUG-1999 (first entry)
 XX
 DE Indolicidin analogue #34.
 XX
 KW Indolicidin; bacterial infection; photo-oxidised solubiliser;
 KW antimicrobial; antibiotic; antiarrhythmic; surrice disinfectant;
 KW additive; shampoo; soap; insecticide; herbicide; preservative;
 KW food; technical material.
 XX
 OS Synthetic.
 XX
 PN WO9807745-A2.
 XX
 PD 26-FEB-1998.
 XX
 PF 21-AUG-1997; 97WO-US14779.
 XX
 PR 13-JAN-1997; 97US-0034949.
 PR 21-AUG-1996; 96US-0024754.
 XX
 PA (MICR-) MICROLOGIX BIOTECH INC.
 XX
 PI Erfle D, Fraser JR, Krieger TJ, Taylor R, West MH;
 XX
 DR WPI: 1998-169090/15.

XX New indolicidin analogues with antimicrobial activity and related
 PT nucleic acid - vectors, transformed cells and antibodies, also
 PT conjugates with polyoxalkylene glycol and fatty acid to reduce
 PT toxicity, useful therapeutically, as disinfectants etc.
 XX

PS Claim 13; Page 89; 129pp; English.

XX AAY24549 to AAY24615 represent indolicidin analogues of formulae
 CC (I)-(VIII) containing up to 25 amino acids (aa): RXXXXZXB (I), BXXXXZXB
 CC (II), BBXXXXZXB (III), BXXXXZXBn(A)nmlBBnGS (IV), BXXXXZBB(A)nM
 CC (V), LBnXnZnXXnXnR (VI), LKXnXZXXnR (VII) and BXXXXZXB (VIII).
 CC Where Z = P or V; X = hydrophobic residue, preferably W; B = basic aa;
 CC preferably R or K; AA = any aa; n = 0 or 1; in (II), at least 1 Z = V;
 CC in (VIII) at least 2 X = F or Y. The analogues are used to treat
 CC infections caused by bacteria (Gram positive or negative, or anaerobic);
 CC fungi (yeast or moulds); parasites (protozoa, nematodes, cestodes or
 CC trematodes) or viruses. Typical of very many pathogens that can be
 CC controlled are *Leishmania*, *Trypanosoma*, *Ascaris lumbricoides*, *Fasciola*
 CC *hepatica*, *Klebsiella pneumoniae*, *Bordetella pertussis*, *Staphylococcus*
 CC *aureus*, *Listeria*, *Clostridium*, rotavirus and papilloma virus. Compounds
 CC derived from the analogues may be used similarly; the compounds may
 CC also be prepared from antibiotics or antiarrhythmic agents. The analogues
 CC may be used therapeutically or to coat medical devices; also they are
 CC useful as surface disinfectants, as additives to shampoo or soaps, as
 CC insecticides or herbicides, or as preservatives for foods and technical
 CC materials. The analogues are administered by injection, lavage, orally
 CC or topically, generally at 0.1-50 mg/Kg. These analogues have a broader
 CC spectrum of activity than indolicidin and modification as compounds
 CC reduces their toxicity.
 CC

XX Sequence 21 AA:
 -50

Query Match 41.1%; Score 99; DB 19; Length 21;
 Best Local Similarity 64.3%; Pred. No. 5.9e-06;
 Matches 18; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

OY 1 ILKKPMPWMPRRKHAEPEAPIMILKK 28
 |||||
 DB 1 ILKKPMPWMPRRKHAEPEAPIMILKK 18

RESULT 7
 AAY91806
 ID AAY91806 standard; peptide; 21 AA.
 AC AAY91806;
 XX
 DT 06-JUN-2000 (first entry)
 XX
 DE Amino acid sequence of cationic peptide MBI 11D4CN.
 XX
 KW Cationic peptide; tumour; pharmaceutical composition; cancer; treatment;
 KW leukaemia; polyoxalkylene-modified; Apo; lymphoma; multiple myeloma;
 KW breast; lung; ovary; cervix; uterus; skin; prostate; liver; colon;
 KW multidrug resistance.
 XX
 OS Synthetic.
 XX
 PN WO9965506-A2.
 XX
 PD 23-DEC-1999.
 XX
 PF 14-JUN-1999; 99WO-CA00552.
 XX
 PR 12-JUN-1998; 98US-0096541.
 XX
 PA (MICR-) MICROLOGIX BIOTECH INC.
 XX
 PI Friedland HD, Krieger TJ, Taylor R, Erfle D, Fraser JR, West MHP;
 XX
 DR WPI: 2000-223549/19.

Novel pharmaceutical composition containing optionally activated polyoxalkylene-modified cationic peptides, useful for treating tumours

Disclosure; Page 15; 94pp; English.

This sequence represents a cationic peptide amino acid sequence, which can be used in the pharmaceutical composition of the invention. The invention relates to a pharmaceutical composition containing at least one activated polyoxalkylene (APO)-modified cationic peptide. The modification of peptides with APO increases their activity against tumour cells, including those with a multidrug resistant phenotype. The pharmaceutical composition can be used to treat tumours, specifically lymphoma, leukaemia, multiple myeloma, or tumours of breast, lung, ovary, cervix, uterus, skin, prostate, liver and colon.

Sequence 21 AA:

Query Match	41.1%	Score 99	DB 21	Length 21
Best Local Similarity	64.3%	Pred. No. 5.9e-06		
Matches 18	Conservative 0	Mismatches 0	Indels 10	Gaps 1

1 ILKKPWWPWRKRHEAPEAPIMILKK 28
1 ILKKPWWPWRKR-----MILKK 18

RESULT 8
AAV24571
ID AAV24571 standard; peptide: 21 AA.

AAV24571:
18-AUG-1999 (first entry)
Indolicidin analogue #23.

Indolicidin; bacterial infection; photo-oxidised solubiliser; antimicrobial; antibiolic; antiarrhythmic; surface disinfectant; additive; shampoo; soap; insecticide; herbicide; preservative; food; technical material.

Synthetic.

WO9807745-A2.
26-FEB-1998.
21-AUG-1997; 97WO-US14779.
13-JAN-1997; 97US-0034949.
21-AUG-1996; 96US-0024754.

(MICR-) MICROLOGIX BIOTECH INC.

Erfile D, Fraser JR, Krieger TJ, Taylor R, West MH;
WPI; 1998-169090/15.

New indolicidin analogues with antimicrobial activity and related nucleic acid - vectors, transformed cells and antibodies, also conjugates with polyoxalkylene glycol and fatty acid to reduce toxicity, useful therapeutically, as disinfectants etc.

Claim 12; Page 89; 129pp; English.

AAV24549 to AAV24615 represent indolicidin analogues of formulae (I)-(VII) containing up to 25 amino acids (aa): Rxxxxxb (I), Bxxxxxb (II), Bbbxxxb (III), Bxxxbbbb (AA), nmilbbags (IV), Bxxxbxb (AA), nm (V), lbbnxxnxxnxxrk (VI), lknxxnxxnxxrk (VII) and Bxxbxxxb (VII). Where z = P or V, x = hydrophobic residue, preferably W; B = basic aa, preferably R or K; AA = any aa; n = 0 or 1; in (II), at least 1 z = V; in (VIII) at least 2 x = F or Y. The analogues are used to treat

CC	infections caused by bacteria (Gram positive or negative, or anaerobic);
CC	fungi (yeast or moulds); parasites (protozoa, nematodes, cestodes or
CC	trematodes) or viruses. Typical of very many pathogens that can be
CC	controlled are Leishmania, Trypanosoma, Ascaris lumbricoides, Fasciola
CC	hepatica, Klebsiella pneumoniae, Bordetella pertussis, Staphylococcus
CC	aureus, Listeria, Clostridium, rotavirus and papilloma virus. Compounds
CC	derived from the analogues may be used similarly; the compounds may
CC	also be prepared from antibiotics or antiarrhythmic agents. The analogues
CC	may be used therapeutically or to coat medical devices; also they are
CC	useful as surface disinfectants, as additives to shampoo or soaps, as
CC	insecticides or herbicides, or as preservatives for foods and technical
CC	materials. The analogues are administered by injection, lavage, orally
CC	or topically, generally at 0.1-50 mg/Kg. These analogues have a broader
CC	spectrum of activity than indolicidin and modification as compounds
CC	reduces their toxicity.
CC	
XX	
SQ	Sequence 21 AA;
OY	Query Match 40.7%; Score 96; DB 19; Length 21; Best Local Similarity 64.3%; Pred. No. 7.8e-06; Matches 18; Conservative 0; Mismatches 0; Indels 10; Gaps 1.
Db	1 ILKKWPMWRKHEAPEAPIMILKK 28 1 ILKKWPMWR-----IMILKK 18
RESULT 9	
AAY91808	AAY91808 standard; Peptide: 21 AA.
XX	
AC	AAY91808;
DF	
DT	06-JUN-2000 (first entry)
XX	
DE	Amino acid sequence of cationic peptide MBI 1ID6CN.
XX	
KM	Cationic peptide; tumour; pharmaceutical composition; cancer; treatment;
KM	Leukaemia; polyoxalkylene-modified; APO; lymphoma; multiple myeloma;
KW	breast; lung; ovary; cervix; uterus; skin; prostate; liver; colon;
KM	multidrug resistance.
XX	
OS	Synthetic.
XX	
PN	WO9965506-A2.
PD	23-DEC-1999.
XX	
PF	14-JUN-1999; 99WO-CA00552.
XX	
PR	12-JUN-1998; 98US-0096541.
XX	
PA	(MICR-) MICROLOGIX BIOTECH INC.
PI	Friedland HD, Krieger TJ, Taylor R, Erfle D, Fraser JR, West MHP,
XX	
DR	WPI: 2000-223549/19.
XX	
PT	Novel pharmaceutical composition containing optionally activated
PT	polyoxalkylene-modified cationic peptides, useful for treating tumours
PS	
PS	Disclosure: Page 15; 94pp; English.
XX	
CC	This sequence represents a cationic peptide amino acid sequence, which
CC	can be used in the pharmaceutical composition of the invention. The
CC	invention relates to a pharmaceutical composition containing at least one
CC	activated polyoxalkylene (APO)-modified cationic peptide. The
CC	modification of peptides with APO increases their activity against tumour
CC	cells, including those with a multidrug resistant phenotype. The
CC	pharmaceutical composition can be used to treat tumours, specifically
CC	lymphoma, leukaemia, multiple myeloma, or tumours of breast, lung, ovary,
CC	cervix, uterus, skin, prostate, liver and colon.

XX Sequence 21 AA; Score 98; DB 21; Length 21;
 SQ Query Match 40.7%; Pred. No. 7.8e-06;
 Best Local Similarity 64.3%; Mismatches 0; Indels 10; Gaps 1;
 Matches 18; Conservative 0; Indels 10; Gaps 1;
 OY 1 ILKKPMPWRRKHEAPEAPIMILKK 28
 |||||
 DB 1 ILKKPMPWRRR-----MILKK 18

RESULT 10
 AAY24570
 ID AAY24570 standard; peptide; 20 AA.
 XX AAY24570;
 AC AAY24570;
 XX 18-AUG-1999 (first entry)
 DT 18-AUG-1999 (first entry)
 DE Indolicidin analogue #22.
 XX Indolicidin; bacterial infection; photo-oxidised solubilisier;
 KM antimicrobial; antibiotic; antiairytumic; surface disinfectant;
 KM additive; shampoo; soap; insecticide; herbicide; preservative;
 KM food; technical material.
 XX Synthetic.
 OS Synthetic.
 XX WO9807745-A2.
 PN WO9807745-A2.
 XX 26-FEB-1998.
 PD 26-FEB-1998.
 XX 21-AUG-1997; 97WO-US14779.
 PF 21-AUG-1997; 97WO-US14779.
 XX 13-JAN-1997; 97US-0034949.
 PR 13-JAN-1997; 97US-0034949.
 XX 21-AUG-1996; 96US-0024754.
 PR 21-AUG-1996; 96US-0024754.
 XX (MICR-) MICROLOGIX BIOTECH INC.
 PA (MICR-) MICROLOGIX BIOTECH INC.
 XX Erlie D. Fraser JR, Krieger TJ, Taylor R, West MH;
 PI Erlie D. Fraser JR, Krieger TJ, Taylor R, West MH;
 XX WPI; 1998-169090/15.
 DR WPI; 1998-169090/15.
 XX New indolicidin analogues with antimicrobial activity and related
 PT nucleic acid vectors, transformed cells and antibodies, also
 PT conjugates with polyoxyalkylene glycol and fatty acid to reduce
 PT toxicity, useful therapeutically, as disinfectants etc.
 XX Claim 12; Page 89; 129pp; English.

AAAY24549 to AAY24615 represent indolicidin analogues of formulae
 CC (I)-(VIII) containing up to 25 amino acids (aa): RXXXXXB (I), RXXXXXB
 CC (II), BXXXXXB (II), BXXXXBBn(AA)nMILBBS (IV), BXXXXBB(AA)nM
 CC (V), LBnXXnXXnXXnXX (VI), LKnXXnXXnXX (VII) and BXXXXXB (VIII).
 CC Where Z = P or V; X = hydrophobic residue, preferably W; B = basic aa,
 CC preferably R or K; AA = any aa; n = 0 or 1; in (II), at least 1 Z = V;
 CC in (VIII) at least 2 X = F or Y. The analogues are used to treat
 CC infections caused by bacteria (Gram positive or negative, or anaerobic);
 CC fungi (yeast or moulds); parasites (protozoa, nematodes, cestodes or
 CC trematodes) or viruses. Typical of very many pathogens that can be
 CC controlled are leishmania, Trypanosoma, Ascaris lumbricoides, Fasciola
 CC hepatica, Klebsiella pneumoniae, Bordetella pertussis, Staphylococcus
 CC aureus, Listeria, Clostridium, rotavirus and papilloma virus. Compounds
 CC derived from the analogues may be used similarly; the compounds may
 CC also be prepared from antibiotics or antiairytumic agents. The analogues
 CC may be used therapeutically or to coat medical devices; also they are
 CC useful as surface disinfectants, as additives to shampoo or soaps, as
 CC insecticides or herbicides, or as preservatives for foods and technical
 CC materials. The analogues are administered by injection, lavage, orally
 CC or topically, generally at 0.1-50 mg/kg. These analogues have a broader
 CC spectrum of activity than indolicidin and modification as compounds
 CC reduces their toxicity.

XX Sequence 20 AA; Score 93.5; DB 19; Length 20;
 SQ Query Match 38.8%; Pred. No. 2.7e-05;
 Best Local Similarity 60.7%; Mismatches 0; Indels 11; Gaps 1;
 Matches 17; Conservative 0; Indels 11; Gaps 1;
 OY 1 ILKKPMPWRRKHEAPEAPIMILKK 28
 |||||
 DB 1 ILKKPMPWRRR-----MILKK 17

RESULT 11
 AAY91807
 ID AAY91807 standard; peptide; 20 AA.
 XX AAY91807;
 AC AAY91807;
 XX 06-JUN-2000 (first entry)
 DT 06-JUN-2000 (first entry)
 DE Amino acid sequence of cationic peptide MBI 11D5CN.
 XX Cationic peptide; tumour; pharmaceutical composition; cancer; treatment;
 KM leukaemia; polyoxyalkylene-modified; Apo; lymphoma; multiple myeloma;
 KM breast; lung; ovary; cervix; uterus; skin; prostate; liver; colon;
 KM multidrug resistance.
 XX Synthetic.
 OS Synthetic.
 XX WO9965506-A2.
 PN WO9965506-A2.
 XX 23-DEC-1999.
 PD 23-DEC-1999.
 XX 14-JUN-1999; 99WO-CA00552.
 PF 14-JUN-1999; 99WO-CA00552.
 XX 12-JUN-1998; 98US-0096541.
 PR 12-JUN-1998; 98US-0096541.
 XX (MICR-) MICROLOGIX BIOTECH INC.
 PA (MICR-) MICROLOGIX BIOTECH INC.
 XX Friedland HD, Krieger TJ, Taylor R, Erlie D, Fraser JR, West MHP;
 PI Friedland HD, Krieger TJ, Taylor R, Erlie D, Fraser JR, West MHP;
 XX WPI; 2000-223549/19.
 DR WPI; 2000-223549/19.
 XX Novel pharmaceutical composition containing optionally activated
 PT polyoxyalkylene-modified cationic peptides, useful for treating tumours
 PT polyoxyalkylene-modified cationic peptides, useful for treating tumours
 PT -
 XX Disclosure; Page 15; 94pp; English.

This sequence represents a cationic peptide amino acid sequence, which
 CC can be used in the pharmaceutical composition of the invention. The
 CC invention relates to a pharmaceutical composition containing at least one
 CC activated polyoxyalkylene (APO)-modified cationic peptide. The
 CC modification of peptides with APO increases their activity against tumour
 CC cells, including those with a multidrug resistant phenotype. The
 CC pharmaceutical composition can be used to treat tumours, specifically
 CC lymphoma, leukaemia, multiple myeloma, or tumours of breast, lung, ovary,
 CC cervix, uterus, skin, prostate, liver and colon.

AAAY12873 to AAY12873 represent indolicidin analogues of formulae
 CC (I)-(VIII) containing up to 25 amino acids (aa): RXXXXXB (I), RXXXXXB
 CC (II), BXXXXXB (II), BXXXXBBn(AA)nMILBBS (IV), BXXXXBB(AA)nM
 CC (V), LBnXXnXXnXXnXX (VI), LKnXXnXXnXX (VII) and BXXXXXB (VIII).
 CC Where Z = P or V; X = hydrophobic residue, preferably W; B = basic aa,
 CC preferably R or K; AA = any aa; n = 0 or 1; in (II), at least 1 Z = V;
 CC in (VIII) at least 2 X = F or Y. The analogues are used to treat
 CC infections caused by bacteria (Gram positive or negative, or anaerobic);
 CC fungi (yeast or moulds); parasites (protozoa, nematodes, cestodes or
 CC trematodes) or viruses. Typical of very many pathogens that can be
 CC controlled are leishmania, Trypanosoma, Ascaris lumbricoides, Fasciola
 CC hepatica, Klebsiella pneumoniae, Bordetella pertussis, Staphylococcus
 CC aureus, Listeria, Clostridium, rotavirus and papilloma virus. Compounds
 CC derived from the analogues may be used similarly; the compounds may
 CC also be prepared from antibiotics or antiairytumic agents. The analogues
 CC may be used therapeutically or to coat medical devices; also they are
 CC useful as surface disinfectants, as additives to shampoo or soaps, as
 CC insecticides or herbicides, or as preservatives for foods and technical
 CC materials. The analogues are administered by injection, lavage, orally
 CC or topically, generally at 0.1-50 mg/kg. These analogues have a broader
 CC spectrum of activity than indolicidin and modification as compounds
 CC reduces their toxicity.

XX AAW12873;
 AC 10-DEC-1997 (first entry)
 DT Antimicrobial cationic peptide CP-11.
 DE
 XX Bacterial; viral; antitumour; food; preservative; inhibitor; growth;
 KM bacterium; yeast; endotoxaemia; sepsis; antibiotic; fungal;
 KW antiviral; Candida albicans; steriliant; Salmonella; yersina;
 KM Shigella.
 OS Synthetic.
 XX WO9708199-A2.
 PN 06-MAR-1997.
 PD
 XX 23-AUG-1996; 96WO-IB00996.
 PF
 XX 23-AUG-1995; 95US-0002687.
 PR (UYBR-) UNIV BRITISH COLUMBIA.
 PA
 XX Falla TJ, Gough M, Hancock RW;
 PI
 XX WPI; 1997-179179/16.
 DR
 XX Cationic peptide(s) having anti-microbial activity - used for the
 PT inhibition of bacterial and viral growth, as an antitumour agent,
 PT and as a food preservative
 PS
 XX Claim 2; Page 65; 89pp; English.
 CC The present sequence represents a specifically claimed novel isolated
 CC cationic peptide which has antimicrobial activity. The amino acid
 CC sequence of antimicrobial cationic peptides (including the present
 CC sequence) is selected from: X1X1PROX2X3X2PRO(X2X2PRO)(X2X3X5)O;
 CC X1X1PROX2X3X4(X5)PROX2X3X3; X1X1X3(ProTyr)uX3X2X5X2X5X2(X5)O;
 CC X1X1X3X3X2PRO(X2X2PRO)(X2X5)m; where m = 1-5; n = 1-2; o = 2-5; r
 CC = 0-6; u = 0-1; X1 = Ile, Leu, Val, Phe, Tyr, Trp or Met; X2 = Trp or
 CC Phe; X3 = Arg or Lys; X4 = Trp or Lys; and X5 = Phe, Trp, Arg, Lys or
 CC Pro. The peptides are preferably amidated or carboxymethylated. The
 CC peptides may be used in methods for inhibiting the growth of a bacterium
 CC or yeast, or for inhibiting an endotoxaemia or sepsis associated
 CC disorder in a subject. The peptides have a broad activity against
 CC antibiotic resistant bacteria, combined with activity against the
 CC medicially important fungus Candida albicans. In addition, the peptides
 CC are useful as antitumour agents and/or antiviral agents. The peptides
 CC may be used as sterilants or preservatives of materials susceptible to
 CC microbial or viral contamination, e.g. in processed foods to inhibit
 CC Salmonella, Yersina and Shigella. The peptides are compact and tend to
 CC have a unique polypyrrolone type II extended helix structure that permits
 CC them to span the membrane with relatively few amino acids. The peptides
 CC possess the ability to work synergistically with antibiotics, and in
 CC addition, some of them possess anti-endotoxin activity.
 CC N.B. The present sequence represents SEQ ID NO:1 in the claims and
 CC examples of the specification, but differs slightly from the SEQ ID NO:1
 CC in the sequence listing on page 51 of the specification (see AAW27179).
 CC
 XX
 SQ Sequence 13 AA;

Query Match 37.8%; Score 91; DB 18; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.5e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ILKKPMPMPWRRK 13
 |||||
 Db 1 ILKKPMPMPWRRK 13

RESULT 13
 AAW24609

ID AAW24609 standard; peptide: 13 AA.
 XX
 AC AAW24609;
 AC 18-AUG-1999 (first entry)
 DT Indolicidin analogue #61.
 DE
 XX Indolicidin; bacterial infection; photo-oxidised solubiliser;
 KM antimicrobial; antibiotic; antitarrhythmic; surface disinfectant;
 KW additive; shampoo; soap; insecticide; herbicide; preservative;
 KM food; technical material.
 OS Synthetic.
 XX WO9807745-A2.
 PN 26-FEB-1998.
 PD
 XX 21-AUG-1997; 97WO-US14779.
 PF
 XX 13-JAN-1997; 97US-0034949.
 PR 21-AUG-1996; 96US-0024754.
 XX (MICR-) MICROLOGIX BIOTECH INC.
 PA
 XX Erfle D, Fraser JR, Krieger TJ, Taylor R, West MH;
 PI
 XX WPI; 1998-169090/15.
 DR
 XX New indolicidin analogues with antimicrobial activity and related
 PT nucleic acid - vectors, transformed cells and antibodies, also
 PT conjugates with polyoxyalkylene glycol and fatty acid to reduce
 PT toxicity, useful therapeutically, as disinfectants etc.
 PS
 XX Example 1; Page 32; 129pp; English.
 CC AAW24549 to AAW24615 represent indolicidin analogues of formulae
 CC (I)-(VIII) containing up to 25 amino acids (aa): RXXXZXB (I), BXXXZXB
 CC (II), BBXXZXB (III), BXZXXZBBn(AA)nmlBBAGS (IV), BXZXXZBB(AA)nM
 CC (V), LBnXZnXZnXRR (VI), LKnXZnXZnRR (VII) and BnXZnXZBB (VIII).
 CC Where Z = P or V; X = hydrophobic residue, preferably W; B = basic aa,
 CC preferably R or K; AA = any aa; n = 0 or 1; in (II), at least 1 Z = V;
 CC in (VIII) at least 2 X = F or Y. The analogues are used to treat
 CC infections caused by bacteria (Gram positive or negative, or anaerobic);
 CC fungi (yeast or moulds); parasites (protozoa, nematodes, cestodes or
 CC trematodes) or viruses. Typical of very many pathogens that can be
 CC controlled are Leishmania, Trypanosoma, Ascaris lumbricoides, Fasciola
 CC hepatica, Klebsiella pneumoniae, Bordetella pertussis, Staphylococcus
 CC aureus, Listeria, Clostridium, rotavirus and papilloma virus. Compounds
 CC derived from the analogues may be used similarly; the compounds may
 CC also be prepared from antibiotics or antitarrhythmic agents. The analogues
 CC may be used therapeutically or to coat medical devices; also they are
 CC useful as surface disinfectants, as additives to shampoo or soaps, as
 CC insecticides or herbicides, or as preservatives for foods and technical
 CC materials. The analogues are administered by injection, lavage, orally
 CC or topically, generally at 0.1-50 mg/kg. These analogues have a broader
 CC spectrum of activity than indolicidin and modification as compounds
 CC reduces their toxicity.
 CC
 XX
 SQ Sequence 13 AA;

Query Match 37.8%; Score 91; DB 19; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.5e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ILKKPMPMPWRRK 13
 |||||
 Db 1 ILKKPMPMPWRRK 13

RESULT 14
 AAW6378

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ID AAW6378 standard; peptide: 13 AA.
XX
AC AAW6378;
XX
DT 12-JAN-1999 (first entry)
XX
DE Cationic peptide of claim 15 #5.
XX
KW Indolicidin analogue; resistance; cationic peptide; antibiotic;
KW bacterial infection; tolerance; antibacterial; microorganism;
KW bacteria; fungus; parasite; virus.
XX
OS Synthetic.
XX
PN WO9840401-A2.
XX
PD 17-SEP-1998.
XX
PF 10-MAR-1998; 98WO-CA00190.
XX
PR 25-FEB-1998; 98US-0030619.
PR 10-MAR-1997; 97US-0040649.
PR 20-AUG-1997; 97US-0915314.
PR 26-SEP-1997; 97US-0060099.
XX
PA (MICR-) MICROLOGIX BIOTECH INC.
XX
PI Fraser JR, McNICOL PJ, West MHP;
XX
DR WPI; 1998-520800/44.
XX
PT New indolicidin peptide analogues - useful for, e.g. enhancing
PT activity of antibiotic or overcoming tolerance; acquired resistance
PT or inherent resistance of microorganisms
XX
PS Claim 15; Page 93; 105pp; English.
XX
CC The present sequence represents a specifically claimed cationic peptide
CC from the present invention. The present invention describes compositions
CC and methods for treating infection, especially bacterial infections. The
CC compositions and methods use cationic peptides in combination with an
CC antibiotic agent which are then administered to a patient to enhance the
CC activity of the antibiotic agent, to overcome: (a) tolerance; (b)
CC acquired resistance; and (c) inherent resistance. The combinations of
CC antibiotics and cationic peptides can provide synergistic activity
CC against a microorganism that is tolerant, inherently resistant, or has
CC acquired resistance to an antibiotic agent. They can be used for killing
CC e.g. bacteria, fungi, parasites and viruses.
XX
SQ Sequence 13 AA;

Query Match 37.8%; Score 91; DB 19; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.5e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILKKPMPWPRRK 13
   |||||||||
Db 1 ILKKPMPWPRRK 13

RESULT 15
AAW71690
ID AAW71690 standard; Peptide: 13 AA.
XX
AC AAW71690;
XX
DT 11-JAN-1999 (first entry)
XX
DE Cationic peptide MB111 (MW 1879).
XX
KW MB111; cationic peptide; plasmid PKL1; small cryptic plasmid;
KW replication; RepA; vector; RAMP.
XX

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OS Synthetic.
XX
PN WO9841636-A2.
XX
PD 24-SEP-1998.
XX
PF 16-MAR-1998; 98WO-CA00214.
XX
PR 14-MAR-1997; 97US-0040722.
XX
PA (BURI/) BURIAN J.
PA (KAYW/) KAY W W.
XX
PI Burian J, Kay WW;
XX
DR WPI; 1998-531571/45.
XX
PT Increasing plasmid copy number in a cell with the repA gene product
PT - and an small cryptic plasmid ori sequence, useful for high level
PT expression of e.g. cytokines, antigens or therapeutic proteins
XX
PS Example 13; Page 54; 82pp; English.
XX
CC MB111 is a small (mol.wt. 1879) cationic peptide. DNA encoding
CC MB111 has been incorporated into vector PR2h-B1, in which the
CC replication leader (R21) sequence of RepA (see also AAW71686) is
CC joined to 2 Hpro peptides (see also AAW71692), to provide a
CC vector for expression of MB111 in host cells. The invention
CC provides controlled replication plasmid vectors (RAMP vectors)
CC comprising a replicated origin of a small cryptic plasmid and a
CC gene encoding RepA. The vectors can reach very high levels of
CC plasmid replication, but are not lethal to the host cell, and can
CC be used to direct the high level expression of e.g. cytokines,
CC antigens and therapeutic proteins.
XX
SQ Sequence 13 AA;

Query Match 37.8%; Score 91; DB 19; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.5e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILKKPMPWPRRK 13
   |||||||||
Db 1 ILKKPMPWPRRK 13

Search completed: December 11, 2002, 15:38:44
Job time : 35 secs

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